

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 10479 Seconds

(without alignments) 10025.556 Million cell updates/sec

Title: US-09-854-867-6

Perfect score: 2760

Sequence: 1 cagtggtctcaactgagcggg.....aaaawgttggaagaccactg 2760

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Search: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_gsa1:*
8: gb_gsa2:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	235.2	8.5	666	9	AG050496 Pan trogl
2	233.4	8.5	497	7	CR737523 CR737523
3	224.8	8.1	668	9	CE769346 Ligr-g88-
4	223	8.1	728	9	CC555035 CH240_461
5	223	8.1	861	9	CC476217 CH240_301
6	220.8	8.0	654	9	CE691282 Ligr-g88-
7	218.4	7.9	627	8	AO506853 RPII-11-2
8	215.4	7.8	622	8	B2883743 CH240_189
9	214.8	7.8	715	5	BQ597867 MT-P-K2-a
10	210.4	7.6	728	9	CE114679 Ligr-g88-
11	207.6	7.5	633	9	CE476563 Ligr-g88-
12	197.4	7.2	701	8	B2867261 CH240_288
13	196	7.1	444	2	AM104660 xds5e03.x
14	191.8	6.9	705	9	CC911866 L068P19ba
15	188.4	6.8	558	8	AO424645 CIRBI-E1-
16	188	6.8	651	9	CLJ01716 gds2_CH25
17	186.4	6.8	754	9	CE328397 Ligr-g88-
18	185.2	6.7	619	8	AO200902 RPII1-61
19	184.8	6.7	583	9	CE667555 Ligr-g88-
20	177.4	6.4	834	7	CK449411 892979 MA
21	173.4	6.3	748	5	BM984741 UI-CF-ECL
22	172.8	6.3	514	1	AI990936 w824g10.x
23	171	6.2	689	8	AO390570 CIRBI-E1-
24	170.2	6.2	448	8	AO197912 CIR-HSP-2

25	170.2	6.2	486	1	AU674187	AU674187
26	170.2	6.2	708	8	B2610828	B2610828
27	169.8	6.2	594	8	AO433787	AO433787
28	169	6.1	487	1	AA024442	AA024442
29	168	6.1	485	9	CE745730	CE745730
30	167.8	6.1	504	8	AO006291	AO006291
31	167	6.1	680	1	AL559202	AL559202
32	167	6.1	680	3	CR624325	CR624325
33	167	6.1	696	6	CA426386	CA426386
34	167	6.1	713	5	BM978242	BM978242
35	167	6.1	1530	3	CR591289	CR591289
36	166.8	6.0	650	8	B59993	B59993
37	166.6	6.0	851	8	B2600766	B2600766
38	165.6	6.0	624	9	CE679167	CE679167
39	165.6	6.0	1071	1	AL539196	AL539196
40	165.2	6.0	858	5	BX392511	BX392511
41	165	6.0	652	8	B2852014	B2852014
42	163.8	5.9	765	6	CB963879	CB963879
43	161.8	5.9	690	5	BM980045	BM980045
44	161.6	5.9	514	8	AO368387	AO368387
45	160.8	5.8	654	8	B2861747	B2861747
46	160.6	5.8	682	8	AO316771	AO316771
47	160	5.8	636	5	BX651581	BX651581
48	159.6	5.8	457	8	AO887234	AO887234
49	159.6	5.8	651	1	AL559201	AL559201
50	158.2	5.7	962	4	BG430553	BG430553
51	157.6	5.7	756	9	CE287618	CE287618
52	157.4	5.7	754	8	AO420143	AO420143
53	155.8	5.6	705	9	CE366279	CE366279
54	155.6	5.6	440	9	CE643311	CE643311
55	155.6	5.6	677	9	CE720006	CE720006
56	155.2	5.6	468	5	BX097159	BX097159
57	155.2	5.6	571	9	CE746991	CE746991
58	155	5.6	629	4	BG567813	BG567813
59	155	5.6	737	5	BUC26144	BUC26144
60	154.8	5.6	649	9	CE503254	CE503254
61	153.8	5.6	701	9	CE025080	CE025080
62	151.6	5.5	755	9	CE437336	CE437336
63	151.6	5.5	892	9	ECAS76604	ECAS76604
64	148.2	5.4	390	8	AO284904	AO284904
65	148.2	5.4	568	8	AO711935	AO711935
66	148.2	5.4	580	8	AO721219	AO721219
67	148	5.4	551	9	CE783887	CE783887
68	147.8	5.4	476	1	AA001539	AA001539
69	147	5.3	834	9	CC473177	CC473177
70	145.4	5.3	497	1	AI424388	AI424388
71	145.4	5.3	533	9	CE212519	CE212519
72	145.4	5.3	537	9	CE768396	CE768396
73	145.4	5.3	602	9	CE625577	CE625577
74	144.2	5.2	3579	3	AK034794	AK034794
75	143.4	5.2	314	7	B8092826	B8092826
76	142.6	5.2	673	2	CE449511	CE449511
77	142.4	5.2	655	9	CE288650	CE288650
78	142.4	5.2	749	9	CR837711	CR837711
79	142.2	5.2	721	7	CR837711	CR837711
80	141.6	5.1	506	9	CE598948	CE598948
81	141.2	5.1	372	8	AO145326	AO145326
82	140.6	5.1	506	1	AI467915	AI467915
83	140	5.1	535	9	CE556591	CE556591
84	140	5.1	535	9	AO403179	AO403179
85	139.8	5.1	573	1	AI768650	AI768650
86	138.2	5.0	765	9	CR836992	CR836992
87	137.8	5.0	545	6	CR854010	CR854010
88	137.4	5.0	615	5	BO714441	BO714441
89	137	5.0	419	8	AO310173	AO310173
90	137	5.0	590	5	BX552227	BX552227
91	135.6	4.9	684	2	BB636408	BB636408
92	135.6	4.9	1090	3	AK041126	AK041126
93	135.2	4.9	463	8	AO083595	AO083595
94	135.2	4.9	699	9	CL350111	CL350111
95	134.2	4.9	830	9	CR130024	CR130024
96	134.2	4.9	697	9	CE558398	CE558398
97	133.2	4.8	753	9	CC925716	CC925716

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 1798.09 Seconds
(without alignments)
9130.760 Million cell updates/sec

Title: US-09-854-867-6
Perfect score: 2760
Sequence: 1 cagtgcttcaactgagggg.....aaaawgttgaagaccatg 2760

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database:

Published Applications NA:
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	US-09-854-867-6	Sequence 6, Appli
2	516.8	18.7	198285	US-09-880-107-3814	Sequence 318, Ap
3	516.8	18.7	198285	US-10-775-169-338	Sequence 318, Ap
4	440.8	16.0	62647	US-10-322-281-274	Sequence 274, Ap
5	400.8	14.5	3673778	US-10-312-841-2	Sequence 2, Appli
6	320	11.6	293625	US-10-719-993-6929	Sequence 1, Appli
7	320	11.6	293625	US-10-087-192-418	Sequence 6929, Ap
8	261	9.5	209484	US-10-331-053-4	Sequence 418, Ap
9	261	9.3	194883	US-10-087-192-826	Sequence 4, Appli
10	256	9.1	53323	US-10-087-192-826	Sequence 826, Ap
11	251	9.1	53323	US-10-741-601-5695	Sequence 5695, Ap

12	251	9.1	53323	19	US-10-741-600-17769	Sequence 17769, A
13	248.6	9.0	78025	14	US-10-020-141-9	Sequence 9, Appli
14	247	8.9	101685	18	US-10-723-860-146	Sequence 146, Ap
15	210.4	7.6	147620	16	US-10-723-860-2768	Sequence 2768, Ap
16	210.2	7.6	72604	16	US-10-162-497-7	Sequence 7, Appli
17	210.2	7.6	72604	16	US-10-629-313-7	Sequence 7, Appli
18	207.2	7.5	12281	19	US-10-741-600-17652	Sequence 17652, A
19	205.2	7.4	3131	13	US-10-027-632-114343	Sequence 114343, A
20	205.2	7.4	3131	13	US-10-027-632-114343	Sequence 114343, A
21	205.2	7.4	3131	13	US-10-027-632-114343	Sequence 114343, A
22	205.2	7.4	3131	17	US-10-027-632-114344	Sequence 114344, A
23	204.4	7.4	1001	17	US-10-294-934-24	Sequence 24, Appli
24	197	7.1	125796	18	US-10-719-993-6804	Sequence 6804, Ap
25	193.4	7.0	15951	15	US-10-311-455-1654	Sequence 1654, Ap
26	193.4	7.0	15951	15	US-10-240-485-134	Sequence 134, Ap
27	190	6.9	17491	15	US-10-240-485-128	Sequence 128, Ap
28	188	6.8	611	13	US-10-027-632-305785	Sequence 305785, A
29	188	6.8	611	13	US-10-027-632-305785	Sequence 305785, A
30	188	6.8	611	17	US-10-027-632-305785	Sequence 305785, A
31	188	6.8	611	17	US-10-027-632-305785	Sequence 305785, A
32	187.4	6.8	42479	18	US-10-719-993-6964	Sequence 6964, Ap
33	187.4	6.8	42479	19	US-10-741-600-17900	Sequence 17900, A
34	187.4	6.8	1980090	18	US-10-719-993-6815	Sequence 6815, Ap
35	187.4	6.8	1980090	19	US-10-741-600-17676	Sequence 17676, A
36	185.8	6.7	96592	11	US-09-997-722-88	Sequence 88, Appli
37	185.2	6.7	15951	15	US-10-311-455-1653	Sequence 1653, Ap
38	185.2	6.7	15951	15	US-10-240-485-133	Sequence 133, Ap
39	176.6	6.4	12079	9	US-09-764-847-1880	Sequence 1880, Ap
40	176.6	6.4	12079	14	US-10-092-154-1880	Sequence 1880, Ap
41	174.6	6.3	40060	18	US-10-388-838-68	Sequence 68, Appli
42	173.4	6.3	554	13	US-10-357-930-5854	Sequence 5854, A
43	169.2	6.1	118931	13	US-10-087-192-1108	Sequence 1108, Ap
44	165.8	6.0	138837	9	US-10-332-281-146	Sequence 146, Ap
45	164.6	6.0	197997	18	US-09-822-246-3	Sequence 3, Appli
46	164.6	6.0	197997	18	US-10-469-028-3	Sequence 3, Appli
47	162	5.9	599	9	US-09-878-722-64	Sequence 64, Appli
48	162	5.9	599	9	US-09-904-456-64	Sequence 64, Appli
49	161.8	5.8	79860	13	US-10-087-192-112	Sequence 112, Ap
50	161.4	5.8	91000	15	US-10-002-491-10	Sequence 10, Appli
51	160	5.8	601	9	US-09-796-692-8236	Sequence 8236, Ap
52	160	5.8	601	14	US-10-040-862-8236	Sequence 8236, Ap
53	160	5.8	601	17	US-10-057-4758-8236	Sequence 8236, Ap
54	160	5.8	601	17	US-10-154-8848-8236	Sequence 8236, Ap
55	160	5.8	601	18	US-10-764-824-8236	Sequence 8236, Ap
56	159.6	5.8	9179	15	US-09-955-866-16	Sequence 16, Appli
57	159.2	5.8	17491	15	US-10-240-485-127	Sequence 127, Ap
58	158.6	5.7	629	13	US-10-027-632-207610	Sequence 207610, A
59	158.6	5.7	629	13	US-10-027-632-207612	Sequence 207612, A
60	158.6	5.7	629	13	US-10-027-632-207612	Sequence 207612, A
61	158.6	5.7	629	17	US-10-027-632-207610	Sequence 207610, A
62	158.6	5.7	629	17	US-10-027-632-207611	Sequence 207611, A
63	158.6	5.7	629	17	US-10-027-632-207612	Sequence 207612, A
64	158.6	5.7	79684	17	US-10-034-650-40	Sequence 40, Appli
65	155	5.6	84539	9	US-09-962-436-36	Sequence 36, Appli
66	153.6	5.6	227931	17	US-10-085-117-274	Sequence 274, Ap
67	153.2	5.6	119472	19	US-10-741-600-17865	Sequence 17865, A
68	153.2	5.6	255015	18	US-10-741-600-17611	Sequence 17611, A
69	152	5.5	120239	19	US-10-322-281-271	Sequence 271, Ap
70	148.4	5.4	676	13	US-10-027-632-196564	Sequence 196564, A
71	148.4	5.4	676	13	US-10-027-632-196564	Sequence 196564, A
72	148.4	5.4	676	17	US-10-027-632-196564	Sequence 196564, A
73	148.4	5.4	676	17	US-10-027-632-196565	Sequence 196565, A
74	148	5.4	98850	18	US-10-719-993-6798	Sequence 6798, Ap
75	147.8	5.4	476	9	US-09-954-456-125	Sequence 125, Ap
76	147.8	5.4	96594	11	US-09-997-722-154	Sequence 154, Ap
77	144.8	5.2	575	13	US-10-027-632-61037	Sequence 61037, A
78	144.8	5.2	575	13	US-10-027-632-61037	Sequence 61037, A
79	144.8	5.2	575	17	US-10-027-632-61037	Sequence 61037, A
80	144.8	5.2	575	17	US-10-027-632-61038	Sequence 61038, A
81	144.8	5.2	577	13	US-10-027-632-109727	Sequence 109727, A
82	144.8	5.2	577	13	US-10-027-632-109728	Sequence 109728, A
83	144.8	5.2	577	17	US-10-027-632-109727	Sequence 109727, A
84	144.8	5.2	577	17	US-10-027-632-109728	Sequence 109728, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 502.914 Seconds
(without alignments)
8979.909 Million cell updates/sec

Title: US-09-854-867-6
Perfect score: 2760
Sequence: 1 cagtgcttcacacacg999.....aaaawgttcgaagaccacg 2760

Scoring table: IDENTITY NNC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB_seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB_seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB_seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB_seq: *
5: /cgn2_6/prodata/1/ina/PCUTUS_COMB_seq: *
6: /cgn2_6/prodata/1/ina/backfillseq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	US-09-573-080A-6	Sequence 6, Appl
2	340.2	12.3	312474	US-09-949-016-17434	Sequence 17434, A
3	262.6	9.5	108169	US-09-949-016-12898	Sequence 12898, A
4	262.6	9.5	108169	US-09-949-016-15907	Sequence 15907, A
5	256	9.3	178884	US-09-949-016-12733	Sequence 12733, A
6	248.6	9.0	45323	US-09-949-016-13039	Sequence 13039, A
7	243.4	8.8	89689	US-09-949-016-16142	Sequence 16142, A
8	215.4	7.8	231129	US-09-949-016-13089	Sequence 13089, A
9	215.4	7.8	266293	US-09-949-016-16110	Sequence 16110, A
10	210.2	7.6	72604	US-09-268-992-7	Sequence 11934, A
11	210.2	7.6	72604	US-09-657-474-7	Sequence 7, Appl
12	205.4	7.4	17730	US-09-949-016-12123	Sequence 12123, A
13	205.4	7.4	17730	US-09-949-016-13472	Sequence 13472, A
14	204.4	7.4	17731	US-09-671-317-24	Sequence 24, Appl
15	204.4	7.3	601	US-09-949-016-148420	Sequence 158420, A
16	201.8	7.1	40951	US-09-949-016-156459	Sequence 156459, A
17	195.4	6.6	83938	US-09-949-016-15668	Sequence 16068, A
18	181.8	6.6	83938	US-09-949-016-15668	Sequence 15947, A
19	177.8	6.4	149543	US-09-949-016-15457	Sequence 15947, A
20	177.8	6.4	80632	US-09-949-016-12951	Sequence 12951, A
21	174.6	6.3	254405	US-09-949-016-14881	Sequence 14881, A
22	172.6	6.3	26134	US-09-949-016-15785	Sequence 15785, A
23	170.6	6.2	253375	US-09-949-016-12849	Sequence 12849, A
24	169.6	6.1	192302	US-09-949-016-15770	Sequence 15770, A
25	167.6	6.1	72128	US-09-949-016-16018	Sequence 16018, A
26	165.2	6.0	145812	US-09-949-016-15698	Sequence 15698, A
27	161.4	5.8	94019	US-09-949-016-13203	Sequence 13203, A

28	161	5.8	601	US-09-949-016-157716	Sequence 157716, A
29	158.6	5.7	63544	US-09-949-016-14025	Sequence 14025, A
30	156.6	5.7	187580	US-09-949-016-12266	Sequence 12266, A
31	156.2	5.7	601	US-09-949-016-52641	Sequence 52641, A
32	155.4	5.6	87216	US-09-949-016-15891	Sequence 15891, A
33	155.2	5.6	601	US-09-949-016-52642	Sequence 52642, A
34	153.4	5.6	294836	US-09-949-016-15974	Sequence 15974, A
35	152.6	5.5	114139	US-09-949-016-15536	Sequence 16536, A
36	149.4	5.4	601	US-09-949-016-159960	Sequence 169960, A
37	148.8	5.4	601	US-09-949-016-122491	Sequence 12491, A
38	148.2	5.4	187595	US-09-949-016-15546	Sequence 15546, A
39	147.8	5.4	601	US-09-949-016-169959	Sequence 169959, A
40	147.6	5.3	450395	US-09-949-016-15473	Sequence 15473, A
41	147.2	5.3	601	US-09-949-016-122450	Sequence 132490, A
42	146.6	5.3	99500	US-09-798-096-10	Sequence 10, Appl
43	146	5.3	601	US-09-949-016-41579	Sequence 41579, A
44	145.6	5.3	601	US-09-949-016-12798	Sequence 12798, A
45	144.8	5.2	45183	US-09-949-016-12798	Sequence 149658, A
46	144.8	5.2	96932	US-09-949-016-17061	Sequence 17061, A
47	144.8	5.2	194537	US-09-949-016-12928	Sequence 12928, A
48	144.8	5.2	201529	US-09-949-016-12740	Sequence 12740, A
49	144.2	5.2	11494	US-09-949-016-13347	Sequence 13347, A
50	143.6	5.2	147321	US-09-949-016-15450	Sequence 15450, A
51	142.8	5.2	1001	US-09-671-317-25	Sequence 25, Appl
52	134.2	4.9	99916	US-09-816-095-3	Sequence 3, Appl
53	132.2	4.8	601	US-09-949-016-157715	Sequence 157715, A
54	131.6	4.8	17607	US-09-949-016-15968	Sequence 15968, A
55	130.6	4.7	19062	US-09-949-016-14877	Sequence 14877, A
56	130.6	4.7	205044	US-09-949-016-15851	Sequence 15851, A
57	130.6	4.7	205044	US-09-949-016-15852	Sequence 15852, A
58	130.6	4.7	205044	US-09-949-016-15853	Sequence 15853, A
59	130.6	4.7	223471	US-09-949-016-12387	Sequence 12387, A
60	130.6	4.7	223471	US-09-949-016-12725	Sequence 12725, A
61	130.6	4.7	223471	US-09-949-016-154471	Sequence 154471, A
62	129.8	4.7	83708	US-09-949-016-17207	Sequence 17207, A
63	129.6	4.7	260247	US-09-949-016-13358	Sequence 13358, A
64	129.6	4.7	601	US-09-949-016-153678	Sequence 153678, A
65	128.8	4.7	24847	US-09-949-016-16086	Sequence 16086, A
66	128.8	4.7	24847	US-09-949-016-16086	Sequence 16086, A
67	127.4	4.6	601	US-09-949-016-17038	Sequence 17038, A
68	127.2	4.6	94830	US-09-949-016-12414	Sequence 12414, A
69	127.2	4.6	94830	US-09-949-016-16336	Sequence 16336, A
70	126.8	4.6	601	US-09-949-016-164030	Sequence 164030, A
71	126.2	4.6	601	US-09-949-016-170385	Sequence 170385, A
72	126.2	4.6	27270	US-09-949-016-13822	Sequence 13822, A
73	125.8	4.6	601	US-09-949-016-12036	Sequence 12036, A
74	124.6	4.5	89843	US-09-949-016-13566	Sequence 13566, A
75	123.4	4.5	89844	US-09-949-016-16566	Sequence 16566, A
76	123.4	4.5	601	US-09-949-016-14547	Sequence 14547, A
77	122.4	4.4	818128	US-09-949-016-14547	Sequence 14547, A
78	122.4	4.4	818128	US-09-949-016-14548	Sequence 14548, A
79	122.4	4.4	818128	US-09-949-016-14549	Sequence 14549, A
80	122.4	4.4	818128	US-09-949-016-14550	Sequence 14550, A
81	122.4	4.4	818128	US-09-949-016-14551	Sequence 14551, A
82	122.4	4.4	818128	US-09-949-016-14552	Sequence 14552, A
83	122.4	4.4	818128	US-09-949-016-14553	Sequence 14553, A
84	122.4	4.4	818128	US-09-949-016-14554	Sequence 14554, A
85	122.4	4.4	818128	US-09-949-016-14555	Sequence 14555, A
86	122.4	4.4	818128	US-09-949-016-14556	Sequence 14556, A
87	122.4	4.4	818128	US-09-949-016-14557	Sequence 14557, A
88	122.4	4.4	818128	US-09-949-016-14558	Sequence 14558, A
89	122.4	4.4	818128	US-09-949-016-14559	Sequence 14559, A
90	122.4	4.4	818128	US-09-949-016-14560	Sequence 14560, A
91	122.4	4.4	818128	US-09-949-016-14561	Sequence 14561, A
92	122.4	4.4	818128	US-09-949-016-14562	Sequence 14562, A
93	122.4	4.4	818128	US-09-949-016-14563	Sequence 14563, A
94	122.4	4.4	818128	US-09-949-016-14564	Sequence 14564, A
95	122.4	4.4	818128	US-09-949-016-14565	Sequence 14565, A
96	122.4	4.4	818128	US-09-949-016-14566	Sequence 14566, A
97	122.4	4.4	818128	US-09-949-016-14567	Sequence 14567, A
98	122.2	4.4	246230	US-09-949-016-17019	Sequence 17019, A
99	122.2	4.4	246230	US-09-949-016-17020	Sequence 17020, A
100	122.2	4.4	246230	US-09-949-016-17021	Sequence 17021, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 1656.86 seconds
(without alignments)
9861.108 Million cell updates/sec

Title: US-09-854-867-6
Perfect score: 2760
Sequence: 1 cagtgcttcaactgacg999.....aaaawgttgaagacactg 2760

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1980s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2716.6	98.4	2760	7	ADSS30973 Human gen
2	516.8	18.7	198285	6	ABK84699 Human CDN
3	516.8	18.7	198285	6	ABN97319 Gene #381
4	516.8	18.7	198285	13	ADRS52987 Drug ther
5	440.8	16.0	62647	13	ABD33246 Human can
6	261	9.5	209484	11	ACN44126 Human gen
7	256	9.3	194883	11	ACN44398 Human gen
8	248.6	9.0	78025	8	ABO77404 Human SEL
9	247	8.9	101685	12	ADQ17329 Osteocarc
10	210.4	7.6	147620	10	ADL13739 Human can
11	210.4	7.6	147620	12	ADQ19948 Human sof
12	210.2	7.6	72604	2	AAZ10752 Genomic s
13	210.2	7.6	72604	6	ABK43231 Human HKN
14	204.4	7.4	1001	3	AAH51133 Human MGS
15	197.6	7.2	2024	4	AAK90504 Human dig
16	195.2	7.1	88892	12	ADQ97695 Human can
17	193.4	7.0	15951	6	ABL34581 Human met
18	193.4	7.0	15951	6	ABL34581 Human met
19	193.4	7.0	15951	6	ABL70374 Chemical
20	193.4	7.0	15951	7	ADSS9842 Complemen

21	190	6.9	17491	6	ABL34575 Human met
22	190	6.9	17491	7	ADSS9836 Complemen
23	189.8	6.9	2026	4	AAK90503 Human dig
24	185.8	6.7	96591	10	ADCS5301 Mouse SOS
25	185.8	6.7	96592	9	ADAB2822 Human SOS
26	185.8	6.7	96592	10	ADB72560 Human SOS
27	185.8	6.7	96592	12	ADM74417 Human car
28	185.2	6.7	15951	6	ABL33680 Human imm
29	185.2	6.7	15951	6	ABL34580 Human met
30	185.2	6.7	15951	6	ABL70373 Chemical
31	185.2	6.7	15951	7	ADSS9841 Bisulphit
32	182.6	6.6	79603	13	ABD32968 7
33	176.6	6.4	12079	4	ABK42993 Genomic s
34	176.6	6.4	12079	9	ADBB1149 Connectiv
35	174.6	6.3	100660	13	ABD32721_3
36	173.4	6.3	554	5	ABV58515 Human pro
37	169.2	6.1	118931	11	ACN44586 Human gen
38	167	6.1	147724	6	ABK83566 Human CDN
39	165.8	6.0	138837	13	ABD33163 Human can
40	165.6	6.0	46366	4	AAK82098 Human imm
41	164.6	6.0	197997	10	AAI54074 Human tra
42	162	5.9	599	6	ABK27627 Human col
43	161.8	5.9	79860	11	ACN44122 Human gen
44	161.4	5.8	91000	9	AAI61326 Human far
45	159.6	5.8	9179	6	ADB36971 Human B7-
46	159.2	5.8	17491	6	ABL34574 Human met
47	159.2	5.8	17491	7	ADSS9835 Bisulphit
48	158.6	5.7	79590	11	ADL27152 Human gen
49	158.6	5.7	79684	9	ADAB3074 Human hCG
50	158.6	5.7	79684	9	ADAB6358 Human hCG
51	158.6	5.7	79684	10	ADB72812 Human hCG
52	157.4	5.7	2020	4	AAK90502 Human dig
53	155	5.6	1359	6	AAI47527 Human DNA
54	155	5.6	84539	6	ABL64158 Stomach c
55	155	5.6	84539	10	ADL13479 Osteocarc
56	152.6	5.5	68940	2	AAK88502 Human chr
57	152	5.5	983	4	AAK88501 Human dig
58	152	5.5	120239	13	ABD33244 Murine ca
59	147.8	5.4	476	6	ABL66415 Lung canc
60	146.6	5.3	96593	10	ADCS5367 Mouse BLM
61	146.6	5.3	96594	9	ADAB2888 Human BLM
62	146.6	5.3	96594	10	ADB72626 Human BLM
63	146.6	5.3	96594	12	ADM74483 Human car
64	146.6	5.3	99500	6	AAI41740 Human REC
65	143.6	5.2	163321	11	ACN43898 Human gen
66	142.8	5.2	1001	3	AAH51134 Human MGS
67	136.8	5.0	4576	8	ABK63703 Human CDN
68	136.8	5.0	56181	12	ADQ97207 Human can
69	136.8	5.0	56181	12	ADQ97207 Human can
70	136.4	4.9	157875	6	ABQ76673 Human CAD
71	136.4	4.9	160820	8	ABQ76673 Human CAD
72	134.2	4.9	99916	6	ADQ3931 Human enz
73	134.2	4.9	116297	12	ADQ97587 Human can
74	131.4	4.8	58952	11	ACN44974 Human gen
75	130	4.7	217409	11	ACN45150 Human gen
76	129.6	4.7	88624	9	AAI62889 Human alp
77	129.6	4.7	277616	13	ABD32602 Human can
78	127.8	4.6	23989	4	AAK72555 Human imm
79	127.8	4.6	27960	4	AAK69779 Human imm
80	127.8	4.6	27960	4	AAK73320 Human imm
81	127.8	4.6	27960	5	AAK73320 Human imm
82	126.6	4.6	27960	5	AAK73320 Human imm
83	126.6	4.6	96593	9	ADAB2885 Mouse BLM
84	126.6	4.6	96593	10	ADB72623 Mouse BLM
85	126.6	4.6	96593	12	ADM74480 Murine ca
86	126.6	4.6	96594	10	ADCS5364 Human Pap
87	120.4	4.4	467	4	AAH88332 CNS disor
88	119.8	4.3	4883	3	AAK79410 Human imm
89	119.8	4.3	4883	3	AAK79410 Human imm
90	119	4.3	301	6	ABN96517 Gene #301
91	118.2	4.3	177851	8	AAI55590 Human sec
92	118.2	4.3	177851	8	AAI55590 Human sec
93	116.6	4.2	4129	9	AAH15429 Human adu
94	116.6	4.2	4129	9	AAH15429 Human adu
95	116.6	4.2	4129	9	AAH15429 Human adu
96	116.6	4.2	4129	9	AAH15429 Human adu
97	116.6	4.2	4129	9	AAH15429 Human adu
98	116.6	4.2	4129	9	AAH15429 Human adu
99	116.6	4.2	4129	9	AAH15429 Human adu
100	116.6	4.2	4129	9	AAH15429 Human adu

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 12660.7 Seconds
(without alignments)
10563.118 Million cell updates/sec

Title: US-09-854-867-6

Perfect score: 2760
Sequence: 1 cagtgctctcaactcggg.....aaaawgttgaagaccactg 2760

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

Genembi: 1: gb ba: 2: gb hgt: 3: gb in: 4: gb om: 5: gb ov: 6: gb pat: 7: gb ph: 8: gb pl: 9: gb pr: 10: gb ro: 11: gb sts: 12: gb sy: 13: gb un: 14: gb vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546.8	19.8	95556	9	CR752645 Human DNA
2	546.8	19.8	95788	9	AL935042 Human DNA
3	546.8	19.8	98309	2	AL671924 Homo sapi
4	546.8	19.8	110856	9	EX927138 Human DNA
5	546.8	19.8	114576	9	EX088556 Human DNA
6	546.8	19.8	118408	9	CR759798 Human DNA
7	546.8	19.8	126988	9	CR759798 Human DNA
8	546.8	19.8	166801	9	AL671681 Human DNA
9	546.8	19.8	175571	2	AC022567 Homo sapi
10	546.8	19.8	217306	2	CR354548 Mus muscu
11	516.8	18.7	198285	6	CQ861705 Sequence
12	516.8	18.7	198285	6	AX411170 Sequence
13	516.8	18.7	198285	9	HSEVMHC
14	486.8	17.6	177726	9	AC148671 Macaca mu
15	485.2	17.6	176807	9	AC148708 Macaca mu
16	444.2	16.1	69248	9	AC002384 Homo sapi
17	442.8	16.0	44670	2	CR762464 Homo sapi
18	440.8	16.0	184302	9	AL162393 Human DNA
19	439.2	15.9	143388	9	AC146122 Pan trogl

20	412.2	14.9	188061	2	AC007373
21	410.4	14.9	163312	9	AC007955
22	410.4	14.9	177172	9	CNS0000G
23	400.8	14.5	34980	6	AX344554
24	400	14.5	154485	2	AC068934
25	400	14.5	164084	9	AP006264
26	400	14.5	172665	2	AC140019
27	400	14.5	197065	9	AC090686
28	371.6	13.5	349980	6	AX344550
29	369.2	13.4	158688	9	AF238380
30	369.2	13.4	171901	2	AC027240
31	369.2	13.4	176364	2	AC126322
32	368.8	13.4	159629	9	AC098616
33	360.6	13.1	195568	9	AC092503
34	360	13.0	133445	2	AC073440
35	360	13.0	170270	2	AP001548
36	360	13.0	174645	9	AC091111
37	360	13.0	175850	2	AP001399
38	360	13.0	194487	2	AP002896
39	360	13.0	204340	2	AC091103
40	358.4	13.0	161674	2	AP001493
41	358.4	13.0	170413	2	AC090405
42	358.4	13.0	186150	2	AP001544
43	356.2	12.9	166715	9	HS30801
44	354.6	12.8	142346	9	AC110992
45	354.6	12.8	146460	2	AC024387
46	354.2	12.8	181745	9	AC008179
47	354.2	12.8	79000	9	AP006295
48	354.2	12.8	180973	9	AC022316
49	352.6	12.8	169248	2	AC145907
50	340.2	12.3	113028	9	HS68D15
51	333.4	12.1	138028	2	AC103743
52	333.4	12.1	164879	9	AC022684
53	333.4	12.1	217659	9	AC116157
54	331.6	12.0	43347	9	AL138734
55	330	12.0	159070	2	AL354939
56	321.6	11.7	67446	2	AL354939
57	320.6	11.6	21533	2	HS352811
58	320	11.6	169986	2	AL353589
59	320	11.6	183104	9	AL355601
60	320	11.6	208026	9	AP006292
61	318.8	11.6	129894	2	AC108181
62	318.8	11.6	138649	2	AC146892
63	318.8	11.3	170543	9	CNS051TC
64	311.6	11.3	209521	2	AC021649
65	311.6	11.3	135855	9	AC098701
66	310.8	11.3	170544	9	AC021012
67	310.8	11.3	170544	9	CNS051TC
68	307.8	11.2	149408	9	AC146272
69	307.8	11.2	171165	9	AC142352
70	306.8	11.1	179844	9	AC009285
71	306.4	11.1	159620	9	AC087069
72	306.4	11.1	167942	9	AC021654
73	303.6	11.0	161874	9	AC114482
74	303.2	11.0	131303	9	AL355974
75	301.8	10.9	141833	9	AL442063
76	301.8	10.9	165904	2	AL158148
77	299.2	10.8	81487	2	HS0770C23
78	298.6	10.8	164908	2	AC012439
79	298.6	10.8	194374	9	AC018667
80	297	10.8	91377	9	AC018667
81	297	10.8	93497	2	AC068009
82	297	10.8	256381	2	AC03610
83	295.4	10.7	94568	9	AC114973
84	295.4	10.7	157751	9	AC016644
85	295.4	10.7	165287	2	AC034165
86	292.8	10.6	143993	9	AC093607
87	292.8	10.6	174274	2	AC044905
88	291.6	10.6	175919	9	AC040918
89	290.6	10.5	100167	9	HS318913
90	288.8	10.5	181013	2	AC148288
91	287.2	10.4	139617	2	AC146889
92	286.6	10.4	24206	9	AC128658

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 1784.41 Seconds
(without alignments)
9130.760 Million cell updates/sec

Title: US-09-854-867-5
Perfect score: 2739
Sequence: 1 cagcggttcctaagtgctg.....aaaagtttgagacgctg 2739

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTOS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2733.2	99.8	2739	10	US-09-854-867-5
2	1304	47.6	1450	10	US-09-854-867-5
3	820.2	29.9	209822	19	US-10-741-600-17560
4	675	24.6	198285	9	US-09-880-107-3814
5	675	24.6	198285	13	US-10-775-169-338
6	597.4	21.8	3451	18	US-10-027-632-115204
7	597.4	21.8	3451	17	US-10-027-632-115204
8	593.6	21.7	31724	13	US-10-087-192-766
9	593.6	21.7	31724	17	US-10-087-192-766
10	590	21.5	75395	17	US-10-331-053-76
11	590	21.5	75395	18	US-10-331-053-76

12	566	20.7	337022	18	US-10-322-696-52	Sequence 52, Appl
13	544.6	19.9	58320	18	US-10-322-281-88	Sequence 88, Appl
14	541.2	19.8	160771	18	US-10-450-826-86	Sequence 86, Appl
15	539.8	19.7	209484	13	US-10-087-192-418	Sequence 418, Appl
16	539.8	19.7	209484	18	US-10-331-053-4	Sequence 4, Appl
17	529.6	19.3	80815	18	US-10-322-281-486	Sequence 486, Appl
18	529	19.3	3352	17	US-10-027-632-115478	Sequence 115478,
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21	520.8	19.0	119472	19	US-10-741-600-17865	Sequence 17865, A
22	504.4	18.4	187844	18	US-10-719-993-6883	Sequence 6883, A
23	503.6	18.4	25950	9	US-09-764-891-597	Sequence 597, Appl
24	503.6	18.4	25950	14	US-10-125-540-597	Sequence 597, Appl
25	503.6	18.4	196686	13	US-10-087-192-484	Sequence 484, Appl
26	503.2	18.4	2756	14	US-09-814-353-20143	Sequence 20143, A
27	503.2	18.4	2756	14	US-10-198-846-9729	Sequence 9729, Ap
28	495.4	18.1	32249	13	US-09-764-891-7477	Sequence 7477, Ap
29	491.6	17.9	228139	13	US-10-087-192-232	Sequence 232, Appl
30	479.8	17.5	414295	18	US-10-719-993-6876	Sequence 6876, Ap
31	479	17.5	85506	17	US-10-085-117-220	Sequence 220, Appl
32	464	16.9	260209	15	US-10-025-966A-23	Sequence 23, Appl
33	456.2	16.7	161531	18	US-10-322-281-252	Sequence 252, Appl
34	456.2	16.7	161531	18	US-10-322-281-252	Sequence 252, Appl
35	449	16.4	62520	18	US-10-266-103-39	Sequence 39, Appl
36	445.6	16.3	15643	9	US-09-764-870-638	Sequence 638, Appl
37	445.6	16.3	15643	14	US-10-125-540-638	Sequence 638, Appl
38	434.4	15.9	66312	13	US-10-087-192-1054	Sequence 1054, Ap
39	424.4	15.5	3179	13	US-10-027-632-113290	Sequence 113290,
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43	417	15.2	350570	18	US-10-417-375-146	Sequence 146, Appl
44	409.8	15.0	98439	19	US-10-741-600-17724	Sequence 17724, A
45	409.8	15.0	112604	18	US-10-723-860-970	Sequence 970, Appl
46	406.6	14.9	3673778	16	US-10-312-841-1	Sequence 1, Appl
47	406.6	14.8	1477	10	US-09-892-877-27	Sequence 27, Appl
48	406.6	14.8	1477	10	US-09-948-783-27	Sequence 27, Appl
49	406.2	14.8	197526	18	US-10-322-281-498	Sequence 498, Appl
50	405.6	14.8	142318	13	US-10-087-192-1504	Sequence 1504, Ap
51	405.2	14.8	177380	19	US-10-484-577-683	Sequence 683, Appl
52	396.2	14.5	161334	13	US-10-087-192-730	Sequence 730, Appl
53	394.2	14.4	3673778	16	US-10-312-841-2	Sequence 2, Appl
54	389.4	14.2	83712	18	US-10-741-601-5705	Sequence 5705, Ap
55	389.4	14.2	83712	19	US-10-052-482-82	Sequence 17805, A
56	384.6	14.0	87878	17	US-10-322-281-54	Sequence 54, Appl
57	382.8	14.0	110877	18	US-10-322-281-54	Sequence 1695, Ap
58	374.8	13.7	21045	9	US-09-764-864-1695	Sequence 1738, Ap
59	373.4	13.6	67810	13	US-10-087-192-1738	Sequence 1960, Ap
60	373	13.6	149612	13	US-10-087-192-1960	Sequence 8382, Ap
61	371.6	13.6	4319	10	US-09-764-891-8382	Sequence 28, Appl
62	371.6	13.6	247682	17	US-10-235-192A-28	Sequence 17611, A
63	370.8	13.5	255015	19	US-10-741-600-17611	Sequence 158, Appl
64	369.8	13.5	32174	9	US-09-908-711-158	Sequence 1134, Ap
65	369.8	13.5	32174	9	US-09-764-860-1134	Sequence 2645, Ap
66	369.8	13.5	32174	9	US-09-764-877-2645	Sequence 232, Appl
67	369.8	13.5	32174	9	US-09-860-670-232	Sequence 6480, Ap
68	369.8	13.5	32174	9	US-09-764-904-90	Sequence 10135, A
69	369.8	13.5	32174	10	US-09-764-891-10135	Sequence 10179, A
70	369.8	13.5	32174	10	US-09-764-891-10179	Sequence 90, Appl
71	369.8	13.5	32174	14	US-10-091-548-90	Sequence 1133, Ap
72	369.8	13.5	32174	14	US-10-074-099-11334	Sequence 1133, Ap
73	369.8	13.5	32174	17	US-10-074-024-609	Sequence 256, Appl
74	369.8	13.5	32174	17	US-10-074-024-609	Sequence 256, Appl
75	369.8	13.5	32174	17	US-10-074-024-609	Sequence 232, Appl
76	369.8	13.5	32174	17	US-10-074-024-609	Sequence 232, Appl
77	369.8	13.5	32174	17	US-10-074-024-609	Sequence 2645, Ap
78	369.8	13.5	32174	17	US-10-074-024-609	Sequence 1769, Ap
79	369	13.5	153382	18	US-10-367-094-179	Sequence 1, Appl
80	363.2	13.3	157875	10	US-09-935-464-1	Sequence 16, Appl
81	363.2	13.3	157875	14	US-10-125-835-1	Sequence 334, Appl
82	363.2	13.3	299598	18	US-10-322-696-16	Sequence 16, Appl
83	362.2	13.0	344548	17	US-10-087-192-334	Sequence 334, Appl
84	354.4	12.9	319608	13	US-10-147-603-1	GENERAL INFORMATION

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 499.088 Seconds
(without alignments)
8979.909 Million cell updates/sec

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Perfect score: 2739
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues.

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2733.2	99.8	2739	4 US-09-573-080A-5	Sequence 5, Appli
2	1304	47.6	1450	4 US-09-573-080A-418	Sequence 418, App
3	901.2	32.9	247239	4 US-09-949-016-17590	Sequence 17590, A
4	820.2	29.9	197131	4 US-09-949-016-12675	Sequence 12675, A
5	820.2	29.9	197131	4 US-09-949-016-17170	Sequence 17170, A
6	629.8	23.0	235064	4 US-09-949-016-15380	Sequence 15380, A
7	597.4	21.8	374159	4 US-09-949-016-15868	Sequence 15868, A
8	590	21.5	75395	4 US-09-984-890-3	Sequence 3, Appli
9	590	21.5	75395	4 US-10-274-194-3	Sequence 3, Appli
10	578.4	21.1	123863	4 US-09-949-016-14202	Sequence 14202, A
11	567.6	20.7	133719	4 US-09-949-016-15092	Sequence 15092, A
12	543.8	19.9	374159	4 US-09-949-016-15868	Sequence 15868, A
13	542.6	19.8	317365	4 US-09-949-016-16001	Sequence 16001, A
14	540.6	19.4	481115	4 US-09-949-016-11940	Sequence 11940, A
15	531.8	19.4	82000	4 US-09-949-016-15595	Sequence 15595, A
16	520.2	19.0	222691	4 US-09-949-016-11762	Sequence 11762, A
17	520.2	19.0	222691	4 US-09-949-016-15842	Sequence 15842, A
18	510.8	18.6	109251	4 US-09-949-016-12530	Sequence 12530, A
19	510.8	18.6	109251	4 US-09-949-016-17321	Sequence 17321, A
20	491.6	17.9	212139	4 US-09-949-016-16065	Sequence 16065, A
21	488.2	17.8	117391	4 US-09-949-016-13945	Sequence 13945, A
22	477.4	17.4	89892	4 US-09-949-016-13667	Sequence 13667, A
23	475.2	17.3	101894	4 US-09-949-016-12005	Sequence 12005, A
24	475.2	17.3	103894	4 US-09-949-016-14450	Sequence 14450, A
25	472.8	17.3	77994	4 US-09-949-016-12517	Sequence 12517, A
26	472.8	17.3	77994	4 US-09-949-016-16021	Sequence 16021, A
27	467.6	17.1	173787	4 US-09-949-016-12542	Sequence 12542, A

28	467.6	17.1	173791	4 US-09-949-016-17302	Sequence 17302, A
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30	452	16.5	55606	4 US-09-949-016-15605	Sequence 15605, A
31	448.8	16.4	91062	4 US-09-949-016-13019	Sequence 13019, A
32	443.6	16.2	232024	4 US-09-949-016-13477	Sequence 13477, A
33	433	15.8	129127	4 US-09-949-016-13481	Sequence 13481, A
34	432.4	15.8	136917	4 US-09-949-016-16369	Sequence 16369, A
35	431	15.7	13675	4 US-09-949-016-11746	Sequence 11746, A
36	428.4	15.6	103447	4 US-09-949-016-15320	Sequence 15320, A
37	421.6	15.4	67755	4 US-09-949-016-18703	Sequence 18703, A
38	419.4	15.3	76165	4 US-09-949-016-12288	Sequence 12288, A
39	419.4	15.3	76165	4 US-09-949-016-14005	Sequence 14005, A
40	415	15.2	99304	4 US-09-949-016-15440	Sequence 15440, A
41	414.8	15.1	237241	4 US-09-949-016-15101	Sequence 15101, A
42	413.6	15.1	95561	4 US-09-949-016-12768	Sequence 12768, A
43	413.6	15.1	95561	4 US-09-949-016-13306	Sequence 13306, A
44	413.6	15.1	95561	4 US-09-949-016-13307	Sequence 13307, A
45	413	15.1	53789	4 US-09-949-016-12137	Sequence 12137, A
46	413	15.1	53789	4 US-09-949-016-13955	Sequence 13955, A
47	406.6	14.8	172677	4 US-09-949-016-13444	Sequence 13444, A
48	406.2	14.8	183202	4 US-09-949-016-13614	Sequence 13614, A
49	405.6	14.8	60141	4 US-09-949-016-15874	Sequence 15874, A
50	400.6	14.6	67181	4 US-09-949-016-13102	Sequence 13102, A
51	396.2	14.5	145320	4 US-09-949-016-15858	Sequence 15858, A
52	395.2	14.4	98708	4 US-09-949-016-13392	Sequence 16392, A
53	390.4	14.3	126468	4 US-09-949-016-14418	Sequence 14418, A
54	390.4	14.3	131724	4 US-09-949-016-12893	Sequence 12893, A
55	384.6	14.0	71879	4 US-09-949-016-17465	Sequence 17465, A
56	382	13.9	168394	4 US-09-949-016-13002	Sequence 13002, A
57	378.2	13.8	55387	4 US-09-949-016-12993	Sequence 12993, A
58	375	13.7	101011	4 US-09-949-016-16933	Sequence 16933, A
59	373	13.6	133613	4 US-09-949-016-15824	Sequence 15824, A
60	369	13.5	147382	4 US-09-949-016-14624	Sequence 14624, A
61	359.2	13.1	44096	4 US-09-949-016-15208	Sequence 15208, A
62	359.2	13.1	81585	4 US-09-949-016-15427	Sequence 15427, A
63	356.2	13.0	421118	4 US-09-949-016-16297	Sequence 16297, A
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65	353.2	12.9	319608	4 US-09-679-409-1	Sequence 1, Appli
66	348	12.7	38052	4 US-09-949-016-13825	Sequence 13825, A
67	345.6	12.6	636591	4 US-09-949-016-11808	Sequence 11808, A
68	345.6	12.6	636591	4 US-09-949-016-13388	Sequence 13388, A
69	344.6	12.6	518	4 US-09-573-080A-419	Sequence 419, App
70	342	12.5	239527	4 US-09-949-016-15980	Sequence 15980, A
71	334.8	12.2	153866	4 US-09-949-016-16919	Sequence 16919, A
72	333.6	12.2	670689	4 US-09-949-016-12305	Sequence 12305, A
73	333.6	12.2	670689	4 US-09-949-016-14207	Sequence 14207, A
74	330.6	12.1	40655	4 US-09-949-016-12032	Sequence 12032, A
75	330.6	12.1	40655	4 US-09-949-016-15919	Sequence 15919, A
76	330.2	12.1	16378	4 US-09-949-016-13510	Sequence 13510, A
77	329.8	12.0	145241	4 US-09-949-016-17394	Sequence 17394, A
78	329.8	12.0	145241	4 US-09-949-016-17395	Sequence 17395, A
79	329.2	12.0	47683	4 US-09-949-016-16460	Sequence 16460, A
80	321.6	11.7	3001	4 US-09-539-333D-115	Sequence 115, App
81	321.6	11.7	3001	4 US-09-539-333D-217	Sequence 217, App
82	319.4	11.7	601	4 US-09-949-016-151738	Sequence 151738, A
83	314	11.5	421118	4 US-09-949-016-16397	Sequence 16397, A
84	312.8	11.4	113538	4 US-09-949-016-16329	Sequence 16329, A
85	311.8	11.4	346112	4 US-09-949-016-13165	Sequence 13165, A
86	308.8	11.3	38705	4 US-09-949-016-13883	Sequence 13883, A
87	308.8	11.3	38705	4 US-09-949-016-13884	Sequence 13884, A
88	306	11.2	114424	4 US-09-949-016-17014	Sequence 17014, A
89	305	11.1	84256	4 US-09-949-016-11775	Sequence 11775, A
90	304.4	11.1	360404	4 US-09-949-016-13173	Sequence 13173, A
91	303.8	11.1	702629	4 US-09-949-016-16224	Sequence 16224, A
92	301.6	11.0	70263	4 US-09-949-016-13375	Sequence 13375, A
93	301.6	11.0	70263	4 US-09-949-016-12748	Sequence 12748, A
94	301.4	11.0	81001	3 US-09-750-580-1	Sequence 1, Appli
95	299.6	10.9	283538	4 US-09-949-016-13506	Sequence 13506, A
96	299.2	10.8	126234	4 US-09-949-016-13541	Sequence 13541, A
97	296	10.6	56832	4 US-09-949-016-12976	Sequence 12976, A
98	293.4	10.7	94593	4 US-09-949-016-16324	Sequence 16324, A
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OM nucleic - nucleic search, using sw model

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9861.108 Million cell updates/sec

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	675	24.6	198285	13	AD852987 Drug ther
6	629.8	22.0	262090	12	AD852987 Drug ther
7	629.8	22.0	262090	12	AD852987 Drug ther
8	593.6	21.5	75395	8	ABX93648 Human gen
9	590	21.5	75395	12	AD852987 Drug ther
10	590	21.5	75395	12	AD852987 Drug ther
11	590	21.5	75395	12	AD852987 Drug ther
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13	550.4	20.1	1613	4	AAK91258 Human dig
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15	548.8	20.0	1613	4	AAK91258 Human dig
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17	544.6	19.9	58320	13	ABD33125 Human can
18	541.2	19.8	160771	6	ABO88179 Human ost
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31	491.6	17.9	228139	11	ACN44002 Human gen
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33	464	16.9	260209	6	AB856564 Human SUL
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56	406.2	14.8	197526	13	ABD33389 Human can
57	405.8	14.8	888	4	AAK64460 Human imm
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64	405.2	14.8	177380	10	AD820870 Human MDR
65	398.2	14.5	21710	4	AAK42185 Human dig
66	396.8	14.5	3647	4	AAK42185 Human dig
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68	396.8	14.5	10117	4	AAK42185 Human dig
69	396.8	14.5	10117	4	AAK42185 Human dig
70	396.2	14.5	161334	11	ACN44334 Human gen
71	394	14.4	110000	10	ADG70447 2
72	394	14.4	110000	10	ADG70447 2
73	393.2	14.4	164772	10	ABZ79565-2
74	391	14.3	2604	8	ABZ79565-2
75	391	14.3	2604	8	ABZ79565-2
76	391	14.3	2604	8	ABZ79565-2
77	384.6	14.0	87878	9	AD820870 Human MDR
78	384.6	14.0	87878	10	AD820870 Human MDR
79	384.6	14.0	87878	10	AD820870 Human MDR
80	384.6	14.0	87878	10	AD820870 Human MDR
81	382.8	14.0	2199	4	AAH17409 Human can
82	378.6	13.8	6512	4	AAK65586 Human imm
83	378.6	13.8	6512	4	AAK65586 Human imm
84	377.8	13.7	21045	6	ABN85746 Human tra
85	374.8	13.7	21045	8	ABX74070 Human nov
86	373.4	13.6	1847	4	AAK70909 Human imm
87	373.4	13.6	1847	4	AAK70909 Human imm
88	373.4	13.6	67810	11	ACN45154 Human gen
89	373.4	13.6	67810	11	ACN45154 Human gen
90	371.6	13.6	4319	12	ADL08109 Human rep
91	371.6	13.6	247682	12	ADL08109 Human rep
92	369.8	13.5	32174	4	AA830638 DNA encod
93	369.8	13.5	32174	4	AA830638 DNA encod

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 12564.4 Seconds
(without alignments)
10563.118 Million cell updates/sec

Title: US-09-854-867-5
Perfect score: 2739
Sequence: 1 cagcggttcctcaagtcgtg.....aaaaagttcgagacgctg 2739

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: GenEmbl: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_cv: *
6: gb_pat: *
7: gb_ph: *
8: gb_pi: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	901.2	32.9 201387	9 HSP12	AL133500 Homo sapi
2	890.4	32.5 212103	9 CNS01DVA	AL133453 Human chr
3	873.6	31.9 127243	9 AL359545	AL135948 Homo sapi
4	873.6	31.9 156799	2 AL359548	AC002417 Homo sapi
5	872	31.8 100839	2 AC004895	AC091194 Homo sapi
6	864.6	31.6 153452	2 AC091194	AL445590 Homo sapi
7	857.4	31.3 201322	9 AC091194	AL445590 Homo sapi
8	839.4	30.6 42418	2 AC015905	AL191825 Human DNA
9	839.4	30.6 186102	2 AC015905	AL191825 Human DNA
10	820.2	29.9 211662	2 AC074394	AF224669 Homo sapi
11	815.4	29.8 202397	2 AC024629	AC074629 Homo sapi
12	787.8	28.7 169650	2 AC024629	AC074629 Homo sapi
13	787.2	28.7 173886	9 HSA17G15	AL009174 Human DNA
14	755	27.6 173886	9 HSA17G15	AL009174 Human DNA
15	747	27.3 124321	9 AC069946	AC069946 Homo sapi
16	706.2	25.8 131185	9 AC069946	AL139343 Human DNA
17	706.2	25.8 144818	9 AC069946	AL139343 Human DNA
18	689	25.2 183774	9 AC079307	AC079307 Homo sapi
19	687.4	25.1 172239	2 AC079307	AC079307 Homo sapi

20	686.6	25.1 186622	2 AC023917	AC023917 Homo sapi
21	678	24.8 95556	9 CR752645	CR752645 Human DNA
22	678	24.8 95788	2 AL935042	AL935042 Homo sapi
23	678	24.8 98309	2 AL671924	AL671924 Homo sapi
24	678	24.8 114576	9 BX088556	BX088556 Human DNA
25	678	24.8 114576	9 CR759798	CR759798 Human DNA
26	678	24.8 118408	9 AL669918	AL669918 Human DNA
27	678	24.8 126988	9 AL671681	AL671681 Human DNA
28	678	24.8 166803	2 AC022567	AC022567 Homo sapi
29	678	24.8 177571	2 CR354548	CR354548 Homo sapi
30	676.4	24.7 110856	6 BX927138	BX927138 Human DNA
31	675	24.7 198285	6 CO861705	CO861705 Sequence
32	675	24.6 198285	6 AX411170	AX411170 Sequence
33	675	24.6 198285	6 HSERMHC	X87344 H. sapiens D
34	665.8	24.3 91774	9 BX321867	BX321867 Human DNA
35	664.6	24.3 39969	2 HSB455L19	AL049590 Human DNA
36	664.6	24.3 208657	2 AC046179	AC046179 Homo sapi
37	662.4	24.1 159969	2 AC093165	AC093165 Homo sapi
38	659.2	24.1 159969	2 AC104791	AC104791 Homo sapi
39	659.2	24.1 189269	2 AP006440	AP006440 Homo sapi
40	650.6	23.8 160966	2 AC148387	AC148387 Rhinolo
41	650.6	23.8 170777	2 AC148444	AC148444 Rhinolo
42	646.8	23.6 157410	2 AC013816	AC013816 Homo sapi
43	645.8	23.6 107166	2 AC080120	AC080120 Homo sapi
44	645.4	23.6 128312	2 AL591885	AL591885 Human DNA
45	641	23.4 9835	9 HSE98F6	282183 Human DNA
46	640.2	23.2 213084	9 HSG164F24	AL050308 Human DNA
47	635.8	23.2 64394	9 AL928596	AL928596 Human DNA
48	629.8	23.0 151977	2 AC015615	AC015615 Homo sapi
49	629.8	23.0 165747	2 AP002340	AP002340 Homo sapi
50	629.8	23.0 202337	2 AC069055	AC069055 Homo sapi
51	625.8	22.8 50988	2 AC104776	AC104776 Homo sapi
52	624.2	22.8 106576	2 AC012666	AC012666 Homo sapi
53	624.2	22.8 176043	2 AC113393	AC113393 Homo sapi
54	624	22.8 109347	2 AL137157	AL137157 Human DNA
55	622.2	22.7 154918	2 HSDJ6788	AL121957 Human DNA
56	622.2	22.7 155362	2 AC022244	AC022244 Homo sapi
57	621.2	22.7 143324	9 AL137881	AL137881 Human DNA
58	619.2	22.6 134060	9 AL358354	AL358354 Human DNA
59	614	22.4 194206	9 AC021863	AC021863 Homo sapi
60	612.8	22.4 155021	2 HS774G10	AL034410 Human DNA
61	612.8	22.4 157357	2 AC025342	AC025342 Homo sapi
62	611.2	22.3 154001	9 AC083904	AC083904 Homo sapi
63	610.6	22.3 130506	9 AC068193	AC068193 Homo sapi
64	610.2	22.3 170059	2 AC136949	AC136949 Homo sapi
65	610.2	22.3 183448	2 AC112131	AC112131 Homo sapi
66	609.6	22.3 135430	2 AC011147	AC011147 Homo sapi
67	609.6	22.3 148517	2 AC011816	AC011816 Homo sapi
68	608.8	22.2 151640	2 CNS06C7P	AL139078 Human chr
69	608.8	22.2 151640	2 AC021373	AC021373 Homo sapi
70	608.6	22.2 119794	9 AC007736	AC007736 Homo sapi
71	608.4	22.2 172476	2 AC067778	AC067778 Homo sapi
72	607	22.2 17967	9 AC026228	AC026228 Homo sapi
73	607	22.2 17967	9 AC027588	AC027588 Homo sapi
74	607	22.2 180480	2 AC025506	AC025506 Homo sapi
75	603	22.0 183547	2 AC009551	AC009551 Homo sapi
76	602.6	22.0 177748	9 AP003781	AP003781 Homo sapi
77	602.6	22.0 197195	9 AP000929	AP000929 Homo sapi
78	601.4	22.0 161871	9 BC018863	BC018863 Homo sapi
79	601.4	22.0 161871	9 BC018863	BC018863 Homo sapi
80	601	21.9 78631	9 AC000057	AC000057 Homo sapi
81	600.2	21.9 151566	2 AC072029	AC072029 Homo sapi
82	598.8	21.9 151470	2 AC137918	AC137918 Homo sapi
83	598.6	21.8 97083	9 AC116345	AC116345 Homo sapi
84	597.4	21.8 44670	2 CR762464	CR762464 Homo sapi
85	596.8	21.8 153152	2 AC104154	AC104154 Pan trogl
86	596.6	21.8 161986	2 AC143302	AC143302 Pan trogl
87	596.6	21.8 163579	2 AC104476	AC104476 Pan trogl
88	596.6	21.8 203249	2 AC151582	AC151582 Pan trogl
89	595.6	21.7 163599	2 AC026041	AC026041 Homo sapi
90	595.6	21.7 163599	2 AC026041	AC026041 Homo sapi
91	595.6	21.7 163599	2 AC026041	AC026041 Homo sapi
92	595.2	21.7 152649	9 AC020651	AC020651 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 1450.35 Seconds
(without alignments)
10025.556 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382

Sequence: 1 ctgcgaacactactctccag.....ctgcctccacatagatc 382

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

EST:*
1: gb_ests1:*
2: gb_ests2:*
3: gb_hnc:*
4: gb_ests3:*
5: gb_ests4:*
6: gb_ests5:*
7: gb_ests6:*
8: gb_ests1:*
9: gb_gses2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303.2	79.4	865	A0741580	HS_5567_B
2	291	76.2	495	A0547254	RPCT-11-4
3	288.8	75.6	730	A0898417	HS_3135_B
4	285.8	74.8	528	B88675	RPCT11-2405
5	274.8	71.9	609	A0424030	CITBI-EI-
6	274.8	71.9	655	A0535220	CITBI-EI-
7	274.8	71.9	673	B0631891	1123f06_Y
8	273.2	71.5	542	A0392576	CITBI-EI-
9	273.2	71.5	754	B0633309	UI-H-EI-
10	270	70.7	422	A0052415	RPCT11-51
11	270	70.7	547	A0506522	RPCT-11-2
12	268.6	70.3	565	A0281715	RPCT11-94
13	268.6	70.3	528	A0520082	RPCT-11-7
14	267.8	70.1	398	A0102208	HS_3035_A
15	266.8	69.8	515	A0118585	HS_3012_A
16	266.8	69.8	565	A0520040	RPCT-11-7
17	266.8	69.8	595	A0201122	RPCT11-46
18	265.4	69.5	426	B73082	RPCT11-11C1
19	263.2	68.9	378	B84447	RPCT11-2405
20	262	68.6	571	A0505941	RPCT-11-2
21	261.4	68.4	506	A0182059	HS_3228_A
22	261.2	68.4	585	A0528503	RPCT-11-3
23	261	68.3	531	A0361200	HS_5038_B
24	261	68.3	663	CB044935	NISC_gc07

25	260.4	68.2	591	A0485537	RPCT-11-2
26	260.4	68.2	656	A0390453	CITBI-EI-
27	260.4	68.2	692	A0542894	RPCT-11-3
28	260.4	68.2	793	CA313369	UI-CF-FNO
29	259.4	67.9	586	A0345530	RPCT11-11
30	258.8	67.7	484	A0507214	RPCT-11-3
31	258.8	67.7	668	A0375147	RPCT11-14
32	258.4	67.6	687	BM992110	UI-H-DEI-
33	257.6	67.4	492	A0206678	HS_3240_A
34	257.2	67.3	675	BM724054	UI-E-EI-
35	256.4	67.1	642	BF508736	UI-H-BI4-
36	256.4	67.1	843	A0749599	HS_5575_A
37	256	67.0	507	A0413561	RPCT-11-1
38	255.8	66.9	540	A0211081	HS_3234_B
39	255.6	66.9	474	A0376719	RPCT11-16
40	255.6	66.9	493	A0374603	RPCT11-16
41	255.6	66.9	559	A0388505	RPCT11-14
42	255.6	66.9	623	A0540002	RPCT-11-3
43	255.4	66.9	578	A0281841	RPCT11-76
44	255.2	66.8	426	A0014220	RPCT11-23
45	254.8	66.7	512	A0148419	HS_3123_A
46	254.2	66.5	478	A0528812	RPCT-11-3
47	254.2	66.5	736	A0527040	CITBI-EI-
48	254	66.5	540	BA477424	DKF2p686H
49	254	66.5	670	AG171695	Pan t1091
50	254	66.5	673	AG146506	Pan t1091
51	253.8	66.4	702	AW976364	EST388473
52	253.2	66.3	522	BI064298	IL3-UT011
53	252.4	66.1	520	A0508451	RPCT-11-2
54	252.4	66.1	821	A0890988	HS_3081_B
55	251.6	65.9	515	BF735890	QV1-K1002
56	251.6	65.8	495	A0319760	RPCT11-10
57	251.2	65.8	589	A0588595	CITBI-EI-
58	250.8	65.7	476	A0720739	HS_5546_B
59	249.8	65.4	981	A0747450	HS_5537_A
60	249.4	65.3	514	A0369065	HS_5022_B
61	249.4	65.3	515	BF929482	IL2-NT020
62	249.4	65.3	589	A0374395	RPCT11-14
63	249.2	65.2	452	A0265445	CITBI-EI-
64	249.2	65.2	657	A0588714	CITBI-EI-
65	249	65.1	466	A0720853	HS_5546_B
66	248.6	65.1	429	BF841742	RC2-H1108
67	248	64.9	554	BX502585	DKF2p779P
68	247.8	64.9	431	W79549	z476f10_r1
69	247.6	64.8	444	A0635356	RPCT-11-4
70	246.6	64.5	489	A0126203	HS_3035_A
71	246.2	64.4	516	A0423497	CITBI-EI-
72	246	64.4	567	A0409149	HS_5066_A
73	246	64.4	567	A0545189	CITBI-EI-
74	245.2	64.2	467	A0428869	CITBI-EI-
75	245.2	64.2	507	A0596757	HS_5206_A
76	245.2	64.2	654	A0423408	CITBI-EI-
77	244.6	64.0	428	W74578	z476f10_r1
78	244.4	64.0	428	A0206677	HS_3240_A
79	244.4	64.0	706	A0782398	HS_3106_A
80	244	63.9	393	A0181082	HS_3218_A
81	243.8	63.8	465	AA7442978	ny15e12.s
82	243.8	63.8	437	A1673314	ts81b01.x
83	243.8	63.8	519	A1635524	ts91d02.x
84	243.8	63.8	664	AG156971	Pan t1091
85	243.8	63.8	844	A0781691	HS_3106_A
86	243.6	63.6	436	A0685236	HS_5515_A
87	243	63.6	521	A0536324	RPCT-11-3
88	242.6	63.5	477	A0335001	HS_5012_B
89	242.4	63.5	565	A0630428	RPCT-11-4
90	242	63.4	582	A0428865	CITBI-EI-
91	242	63.4	603	A0590605	HS_5398_A
92	241.8	63.3	521	A0753922	RPCT-11-2
93	241.8	63.3	560	A0508987	RPCT-11-2
94	241.6	63.2	441	A0377070	RPCT11-15
95	241.2	63.1	557	A0734463	HS_3012_A
96	241.2	63.1	852	A0751469	HS_5568_B
97	240.4	62.9	396	A0534062	RPCT-11-3

A0485537	RPCT-11-2
A0390453	CITBI-EI-
A0542894	RPCT-11-3
CA313369	UI-CF-FNO
A0345530	RPCT11-11
A0507214	RPCT-11-3
A0375147	RPCT11-14
BM992110	UI-H-DEI-
A0206678	HS_3240_A
BM724054	UI-E-EI-
BF508736	UI-H-BI4-
A0749599	HS_5575_A
A0413561	RPCT-11-1
A0211081	HS_3234_B
A0376719	RPCT11-16
A0374603	RPCT11-16
A0388505	RPCT11-14
A0540002	RPCT-11-3
A0281841	RPCT11-76
A0014220	RPCT11-23
A0148419	HS_3123_A
A0528812	RPCT-11-3
A0527040	CITBI-EI-
BA477424	DKF2p686H
AG171695	Pan t1091
AG146506	Pan t1091
AW976364	EST388473
BI064298	IL3-UT011
A0508451	RPCT-11-2
A0890988	HS_3081_B
BF735890	QV1-K1002
A0319760	RPCT11-10
A0588595	CITBI-EI-
A0720739	HS_5546_B
A0747450	HS_5537_A
A0369065	HS_5022_B
BF929482	IL2-NT020
A0374395	RPCT11-14
A0265445	CITBI-EI-
A0588714	CITBI-EI-
A0720853	HS_5546_B
BF841742	RC2-H1108
BX502585	DKF2p779P
W79549	z476f10_r1
A0635356	RPCT-11-4
A0126203	HS_3035_A
A0423497	CITBI-EI-
A0409149	HS_5066_A
A0545189	CITBI-EI-
A0428869	CITBI-EI-
A0596757	HS_5206_A
A0423408	CITBI-EI-
W74578	z476f10_r1
A0206677	HS_3240_A
A0782398	HS_3106_A
A0181082	HS_3218_A
AA7442978	ny15e12.s
A1673314	ts81b01.x
A1635524	ts91d02.x
AG156971	Pan t1091
A0781691	HS_3106_A
A0685236	HS_5515_A
A0536324	RPCT-11-3
A0335001	HS_5012_B
A0630428	RPCT-11-4
A0428865	CITBI-EI-
A0590605	HS_5398_A
A0753922	RPCT-11-2
A0508987	RPCT-11-2
A0377070	RPCT11-15
A0734463	HS_3012_A
A0751469	HS_5568_B
A0534062	RPCT-11-3

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 248.866 Seconds
(without alignments)
9130.760 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382
Sequence: 1 ctgcagacactactccag.....ctgtccctccatcagatc 382

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	US-09-854-867-4	Sequence 4, App1
2	364.4	95.4	1959	US-09-864-761-3814	Sequence 3814, Ap
3	306.6	80.3	538	US-10-027-632-235922	Sequence 235922,
4	306.6	80.3	538	US-10-027-632-235923	Sequence 235923,
5	306.6	80.3	538	US-10-027-632-235924	Sequence 235924,
6	306.6	80.3	538	US-10-027-632-235925	Sequence 235925,
7	306.6	80.3	538	US-10-027-632-235926	Sequence 235926,
8	306.6	80.3	538	US-10-027-632-235927	Sequence 235927,
9	278.6	72.9	1002	US-10-029-386-25469	Sequence 25469, A
10	274.8	71.9	2771	US-10-104-047-1081	Sequence 1081, Ap
11	267.4	70.0	672	US-09-864-761-20580	Sequence 20580, A

C 12	260.4	68.2	509	9	US-09-864-761-18463	Sequence 18463, A
C 13	260.4	68.2	575	16	US-10-029-386-1189	Sequence 1189, Ap
C 14	255.6	66.9	525	16	US-10-029-386-3654	Sequence 3654, Ap
C 15	255.6	66.9	591	16	US-10-029-386-3599	Sequence 3599, Ap
C 16	255	66.8	505	16	US-10-029-386-3729	Sequence 3729, Ap
C 17	254	66.5	624	13	US-10-027-632-193860	Sequence 193860,
C 18	254	66.5	624	17	US-10-027-632-193860	Sequence 193860,
C 19	250.8	65.7	527	9	US-09-864-761-8023	Sequence 8023, Ap
C 20	248.8	65.1	524	16	US-10-029-386-11769	Sequence 11769, A
C 21	248.2	65.0	572	16	US-10-029-386-22602	Sequence 22602, A
C 22	246.6	64.6	542	16	US-10-029-386-6571	Sequence 6571, Ap
C 23	246.2	64.5	560	13	US-10-027-632-238047	Sequence 238047,
C 24	246.2	64.5	560	13	US-10-027-632-238048	Sequence 238048,
C 25	246.2	64.5	560	13	US-10-027-632-238049	Sequence 238049,
C 26	246.2	64.5	560	13	US-10-027-632-238050	Sequence 238050,
C 27	246.2	64.5	560	17	US-10-027-632-238047	Sequence 238047,
C 28	246.2	64.5	560	17	US-10-027-632-238048	Sequence 238048,
C 29	246.2	64.5	560	17	US-10-027-632-238049	Sequence 238049,
C 30	246.2	64.5	560	17	US-10-027-632-238050	Sequence 238050,
C 31	245.6	64.3	492	9	US-09-864-761-1708	Sequence 1708, Ap
C 32	242.8	63.6	454	16	US-10-029-386-20535	Sequence 20535, A
C 33	242.8	63.6	1055	16	US-10-029-386-22726	Sequence 22726, A
C 34	242.4	63.5	438	13	US-10-027-632-183614	Sequence 183614,
C 35	242.4	63.5	438	13	US-10-027-632-183615	Sequence 183615,
C 36	242.4	63.5	438	13	US-10-027-632-183616	Sequence 183616,
C 37	242.4	63.5	438	17	US-10-027-632-183614	Sequence 183614,
C 38	242.4	63.5	438	17	US-10-027-632-183615	Sequence 183615,
C 39	242.4	63.5	438	17	US-10-027-632-183616	Sequence 183616,
C 40	241.2	63.1	496	16	US-10-029-386-20296	Sequence 20296, A
C 41	241.2	63.1	521	16	US-10-029-386-11765	Sequence 11765, A
C 42	241.2	63.1	530	13	US-10-027-632-60201	Sequence 60201, A
C 43	241.2	63.1	530	13	US-10-027-632-60202	Sequence 60202, A
C 44	241.2	63.1	530	13	US-10-027-632-60203	Sequence 60203, A
C 45	241.2	63.1	853	16	US-10-029-386-25323	Sequence 25323, A
C 46	241	63.1	504	13	US-10-027-632-214204	Sequence 214204, A
C 47	241	63.1	504	13	US-10-027-632-214205	Sequence 214205,
C 48	241	63.1	504	17	US-10-027-632-214204	Sequence 214204,
C 49	241	63.1	504	17	US-10-027-632-214205	Sequence 214205,
C 50	238.8	62.5	637	13	US-10-027-632-245373	Sequence 245373,
C 51	238.8	62.5	637	13	US-10-027-632-245374	Sequence 245374,
C 52	238.8	62.5	637	17	US-10-027-632-245373	Sequence 245373,
C 53	238.8	62.5	637	17	US-10-027-632-245374	Sequence 245374,
C 54	238.4	62.4	546	13	US-10-027-632-194756	Sequence 194756,
C 55	238.4	62.4	546	13	US-10-027-632-194757	Sequence 194757,
C 56	238.4	62.4	546	13	US-10-027-632-194758	Sequence 194758,
C 57	238.4	62.4	546	17	US-10-027-632-194757	Sequence 194757,
C 58	238.4	62.4	546	17	US-10-027-632-194758	Sequence 194758,
C 59	238.4	62.4	546	17	US-10-027-632-194759	Sequence 194759,
C 60	237.2	62.1	581	13	US-10-027-632-95663	Sequence 95663, A
C 61	237.2	62.1	581	13	US-10-027-632-95664	Sequence 95664, A
C 62	237.2	62.1	581	13	US-10-027-632-95665	Sequence 95665, A
C 63	237.2	62.1	581	13	US-10-027-632-95666	Sequence 95666, A
C 64	237.2	62.1	581	13	US-10-027-632-95667	Sequence 95667, A
C 65	237.2	62.1	581	13	US-10-027-632-95668	Sequence 95668, A
C 66	237.2	62.1	581	13	US-10-027-632-95669	Sequence 95669, A
C 67	237.2	62.1	581	17	US-10-027-632-95663	Sequence 95663, A
C 68	237.2	62.1	581	17	US-10-027-632-95664	Sequence 95664, A
C 69	237.2	62.1	581	17	US-10-027-632-95665	Sequence 95665, A
C 70	237.2	62.1	581	17	US-10-027-632-95666	Sequence 95666, A
C 71	237.2	62.1	581	17	US-10-027-632-95667	Sequence 95667, A
C 72	236.8	62.0	595	13	US-10-027-632-221958	Sequence 221958,
C 73	236.8	62.0	595	13	US-10-027-632-221959	Sequence 221959,
C 74	236.8	62.0	595	17	US-10-027-632-221958	Sequence 221958,
C 75	236.8	62.0	595	17	US-10-027-632-221959	Sequence 221959,
C 76	236.4	61.9	2896	17	US-10-108-2604-987	Sequence 987, App
C 77	236	61.8	533	13	US-10-027-632-80624	Sequence 80624, A
C 78	236	61.8	533	13	US-10-027-632-80625	Sequence 80625, A
C 79	234.8	61.5	532	16	US-10-029-386-9239	Sequence 9239, Ap
C 80	233.6	61.2	520	13	US-10-027-632-248095	Sequence 248095,
C 81	233.6	61.2	520	13	US-10-027-632-248096	Sequence 248096,
C 82	233.6	61.2	520	13	US-10-027-632-248097	Sequence 248097,
C 83	233.6	61.2	520	17	US-10-027-632-248095	Sequence 248095,
C 84	233.6	61.2	520	17	US-10-027-632-248096	Sequence 248096,

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 69.6062 Seconds

(without alignments)
8979.909 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382
Sequence: 1 ctgcagacactactccag.....ctgtccctcacatagaattc 382

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	4	US-09-573-080A-4
2	38.4	10.1	83617	4	US-09-949-016-12254
3	38	9.9	36223	4	US-09-949-016-14417
4	35.2	9.2	2407	4	US-09-023-655-812
5	33.2	8.7	221958	4	US-09-949-016-12173
6	33.2	8.7	221966	4	US-09-949-016-15498
7	32.6	8.5	43018	4	US-09-949-016-12265
8	32.6	8.5	43095	4	US-09-949-016-17530
9	32.4	8.5	957	3	US-09-123-912-113
10	32.4	8.5	957	3	US-09-643-597-113
11	32.4	8.5	957	4	US-09-480-884A-113
12	32.4	8.5	957	4	US-09-542-615A-113
13	32.4	8.5	957	4	US-09-606-421B-113
14	32.4	8.5	957	4	US-09-221-107-113
15	32.4	8.5	957	4	US-09-466-396A-113
16	32.4	8.5	957	4	US-09-476-496A-113
17	32.4	8.5	957	4	US-09-630-940B-113
18	32.4	8.5	957	4	US-09-285-479-113
19	32.4	8.5	1497	4	US-09-230-132-94
20	32.4	8.5	58356	4	US-09-949-016-15553
21	32.2	8.4	601	4	US-09-949-016-12691
22	32.2	8.4	601	4	US-09-949-016-12693
23	32.2	8.4	137394	4	US-09-949-016-12872
24	32.2	8.4	137743	4	US-09-949-016-12178
25	31.8	8.3	601	4	US-09-949-016-12692
26	31.8	8.3	118143	4	US-09-949-016-17196
27	31.6	8.3	601	4	US-09-949-016-15068

28	31.6	8.3	28358	4	US-09-949-016-13506	Sequence 13506, A
29	31.4	8.2	60110	4	US-09-949-016-17338	Sequence 17338, A
30	31.4	8.2	60110	4	US-09-949-016-17339	Sequence 17339, A
31	31.4	8.2	61083	4	US-09-949-016-14144	Sequence 14144, A
32	31.4	8.2	61083	4	US-09-949-016-14145	Sequence 14145, A
33	31.2	8.2	601	4	US-09-949-016-179097	Sequence 179097, A
34	31.2	8.2	13595	4	US-09-949-016-12529	Sequence 12529, A
35	31.2	8.2	13970	4	US-09-949-016-16590	Sequence 16590, A
36	31.2	8.2	59479	4	US-09-949-016-16910	Sequence 16910, A
37	31	8.1	382	4	US-09-573-080A-4	Sequence 4, Appl
38	31	8.1	601	4	US-09-949-016-68262	Sequence 68262, A
39	31	8.1	601	4	US-09-949-016-68263	Sequence 68263, A
40	31	8.1	132456	4	US-09-949-016-17350	Sequence 17350, A
41	31	8.1	247299	4	US-09-949-016-17590	Sequence 17590, A
42	30.6	8.0	19826	4	US-09-949-016-16973	Sequence 16973, A
43	30.6	8.0	28198	4	US-09-949-016-12349	Sequence 12349, A
44	30.6	8.0	14635	4	US-09-949-016-13927	Sequence 13927, A
45	30.2	7.9	15478	4	US-09-949-016-12529	Sequence 12529, A
46	30.2	7.9	15478	4	US-09-949-016-15288	Sequence 15288, A
47	30	7.9	601	4	US-09-949-016-198083	Sequence 198083, A
48	30	7.9	2376	1	US-07-912-952-3	Sequence 3, Appl
49	30	7.9	24020	4	US-09-949-016-17353	Sequence 17353, A
50	29.8	7.8	31623	4	US-09-949-016-15945	Sequence 15945, A
51	29.8	7.8	56678	4	US-09-949-016-17453	Sequence 17453, A
52	29.8	7.8	149543	4	US-09-949-016-17573	Sequence 17573, A
53	29.6	7.7	322	4	US-09-513-999C-17698	Sequence 17698, A
54	29.6	7.7	601	4	US-09-949-016-120621	Sequence 120621, A
55	29.6	7.7	18349	4	US-09-949-016-14463	Sequence 14463, A
56	29.6	7.7	145812	4	US-09-949-016-15698	Sequence 15698, A
57	29.6	7.7	209210	4	US-09-949-016-15094	Sequence 15094, A
58	29.4	7.7	601	4	US-09-949-016-37902	Sequence 37902, A
59	29.4	7.7	601	4	US-09-949-016-142690	Sequence 142690, A
60	29.4	7.7	1844	3	US-09-123-912-88	Sequence 88, Appl
61	29.4	7.7	1844	3	US-09-643-597-88	Sequence 88, Appl
62	29.4	7.7	1844	4	US-09-542-615A-88	Sequence 88, Appl
63	29.4	7.7	1844	4	US-09-606-421B-88	Sequence 88, Appl
64	29.4	7.7	1844	4	US-09-476-496A-88	Sequence 88, Appl
65	29.4	7.7	1844	4	US-09-466-396A-88	Sequence 88, Appl
66	29.4	7.7	1844	4	US-09-476-496A-88	Sequence 88, Appl
67	29.4	7.7	1844	4	US-09-630-940B-88	Sequence 88, Appl
68	29.4	7.7	1844	4	US-09-285-479-88	Sequence 88, Appl
69	29.4	7.7	1844	4	US-09-865-662E-7	Sequence 7, Appl
70	29.4	7.7	3134	3	US-08-374-219B-7	Sequence 7, Appl
71	29.4	7.7	32721	4	US-09-949-016-151400	Sequence 151400, A
72	29.4	7.7	90618	4	US-09-949-016-15964	Sequence 15964, A
73	29.4	7.7	112705	4	US-09-949-016-15630	Sequence 15630, A
74	29.4	7.7	112705	4	US-09-949-016-12632	Sequence 12632, A
75	29.4	7.7	112705	4	US-09-949-016-15775	Sequence 15775, A
76	29.4	7.7	112705	4	US-09-949-016-173529	Sequence 173529, A
77	29.2	7.6	601	4	US-09-949-016-143710	Sequence 143710, A
78	29.2	7.6	601	4	US-09-949-016-15956	Sequence 15956, A
79	29.2	7.6	601	4	US-09-949-016-15957	Sequence 15957, A
80	29.2	7.6	55135	4	US-09-949-016-15887	Sequence 15887, A
81	29.2	7.6	69199	4	US-09-949-016-13881	Sequence 13881, A
82	29.2	7.6	421491	4	US-09-949-016-12805	Sequence 12805, A
83	29.2	7.6	421494	4	US-09-949-016-14060	Sequence 14060, A
84	29.2	7.6	601	4	US-09-949-016-144402	Sequence 144402, A
85	29	7.6	601	4	US-09-387-286-57	Sequence 57, Appl
86	29	7.6	45289	4	US-09-949-016-13228	Sequence 13228, A
87	29	7.6	105050	4	US-09-949-016-15953	Sequence 15953, A
88	29	7.6	133613	4	US-09-949-016-15824	Sequence 15824, A
89	29	7.6	174170	4	US-09-949-016-14810	Sequence 14810, A
90	29	7.6	174170	4	US-09-949-016-14811	Sequence 14811, A
91	29	7.6	174170	4	US-09-949-016-14812	Sequence 14812, A
92	29	7.6	174170	4	US-09-949-016-14813	Sequence 14813, A
93	29	7.6	174170	4	US-09-949-016-14814	Sequence 14814, A
94	29	7.6	174170	4	US-09-949-016-14815	Sequence 14815, A
95	29	7.6	174170	4	US-09-949-016-14816	Sequence 14816, A
96	29	7.6	174170	4	US-09-949-016-14817	Sequence 14817, A
97	28.8	7.5	453	4	US-09-543-681A-4017	Sequence 4017, Ap
98	28.8	7.5	601	4	US-09-949-016-32510	Sequence 32510, A
99	28.8	7.5	601	4	US-09-949-016-32511	Sequence 32511, A
100	28.8	7.5	601	4	US-09-949-016-32511	Sequence 32511, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 229.319 Seconds

(without alignments)
9861.108 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382
Sequence: 1 ctgcagacactactccag.....ctgcctccatcgaattc 382

Scoring table:

IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

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4: geneeqn2000s:*
5: geneeqn2001as:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	7	AD530971 Human gen
2	364.4	95.4	1959	4	AA135309 Probe #39
3	364.4	95.4	1959	4	ABA45170 Human bre
4	364.4	95.4	1959	4	ABA25348 Probe #38
5	364.4	95.4	1959	4	AAK03877 Human bra
6	364.4	95.4	1959	6	AB528968 Human liv
7	364.4	95.4	1959	6	AB503907 Human gen
8	278.6	72.9	1002	12	ACH92274 Human gen
9	278.6	72.9	6477	5	AA568898 DNA encod
10	274.8	71.9	2771	10	ADB62927 Human gen
11	267.4	70.0	672	4	AA148466 Probe #17
12	267.4	70.0	672	4	ABA50306 Human bre
13	267.4	70.0	672	4	ABA53260 Probe #13
14	267.4	70.0	672	4	AAK16627 Human bra
15	267.4	70.0	672	4	ABA41996 Human liv
16	267.4	70.0	672	6	AB516442 Human gen
17	260.4	68.2	509	4	AA120995 Probe #10
18	260.4	68.2	509	4	ABA66063 Human foe
19	260.4	68.2	509	4	AA16244 Probe #14
20	260.4	68.2	509	4	ABA48185 Human bre

C	21	260.4	68.2	509	4	ABA33143	ABA33143 Probe #11
C	22	260.4	68.2	509	4	AAK40229	AAK40229 Human bon
C	23	260.4	68.2	509	4	AAK14487	AAK14487 Human bra
C	24	260.4	68.2	509	4	AB539806	AB539806 Human liv
C	25	260.4	68.2	509	5	AA106707	AA106707 Probe #66
C	26	260.4	68.2	509	6	AB514270	AB514270 Human gen
C	27	260.4	68.2	575	12	ACH67994	ACH67994 Human gen
C	28	260.4	68.2	2436	5	AA570526	AA570526 DNA encod
C	29	256.2	67.1	2448	5	AA567750	AA567750 DNA encod
C	30	255.8	67.0	756	12	ADN99992	ADN99992 Novel hum
C	31	255.8	67.0	756	12	ADN98424	ADN98424 Novel hum
C	32	255.6	66.9	525	12	ACH70459	ACH70459 Human gen
C	33	255.6	66.9	525	12	ACH70404	ACH70404 Human gen
C	34	255.6	66.8	505	12	ACH70534	ACH70534 Human gen
C	35	254	66.5	1055	5	AA569705	AA569705 DNA encod
C	36	250.8	65.7	527	4	ABA52174	ABA52174 Human foe
C	37	250.8	65.7	527	4	AA142128	AA142128 Probe #10
C	38	250.8	65.7	527	4	ABA29557	ABA29557 Probe #80
C	39	250.8	65.7	527	4	AAK36394	AAK36394 Human bon
C	40	250.8	65.7	527	4	AAK10495	AAK10495 Human bra
C	41	250.8	65.7	527	4	AB536069	AB536069 Human liv
C	42	248.8	65.1	524	12	ACH78574	ACH78574 Human gen
C	43	248.2	65.0	572	12	ACH89407	ACH89407 Human gen
C	44	246.6	64.6	542	12	ACH73376	ACH73376 Human gen
C	45	245.6	64.3	492	4	AA111783	AA111783 Probe #17
C	46	245.6	64.3	492	4	ABA53473	ABA53473 Human foe
C	47	245.6	64.3	492	4	AA133095	AA133095 Probe #17
C	48	245.6	64.3	492	4	ABA43059	ABA43059 Human bre
C	49	245.6	64.3	492	4	ABA23242	ABA23242 Probe #17
C	50	245.6	64.3	492	4	AAK27200	AAK27200 Human bon
C	51	245.6	64.3	492	4	AAK01745	AAK01745 Human bra
C	52	245.6	64.3	492	4	AB526780	AB526780 Human liv
C	53	245.6	64.3	492	5	AA101712	AA101712 Probe #17
C	54	245.6	64.3	492	5	AB501743	AB501743 Human gen
C	55	244.4	64.0	1342	5	AA570666	AA570666 DNA encod
C	56	242.8	63.6	454	12	ACH87340	ACH87340 Human gen
C	57	242.8	63.6	1055	12	ACH89531	ACH89531 Human gen
C	58	241.2	63.1	496	12	ACH87103	ACH87103 Human gen
C	59	241.2	63.1	521	12	ACH78570	ACH78570 Human gen
C	60	241.2	63.1	832	12	ACH92128	ACH92128 Human gen
C	61	241.2	63.1	833	12	ACH89745	ACH89745 Human gen
C	62	238.8	62.5	965	5	AA580774	AA580774 DNA encod
C	63	236.4	61.9	2896	11	ADM02302	ADM02302 Human gen
C	64	234.8	61.5	532	12	ACH76044	ACH76044 Human gen
C	65	233.2	61.0	615	12	ACH92054	ACH92054 Human gen
C	66	232.8	60.9	882	12	ACH89517	ACH89517 Human gen
C	67	231.2	60.5	1002	12	ADN99993	ADN99993 Novel hum
C	68	231.2	60.5	1002	12	ADN98425	ADN98425 Novel hum
C	69	231.2	60.5	386	4	ABA74668	ABA74668 Human foe
C	70	231	60.5	386	4	AA155161	AA155161 Probe #23
C	71	231	60.5	386	4	ABA39407	ABA39407 Probe #17
C	72	231	60.5	386	4	AAK49314	AAK49314 Human bon
C	73	231	60.5	386	4	AAK23141	AAK23141 Human bra
C	74	231	60.5	386	4	AB548953	AB548953 Human liv
C	75	230	59.8	519	12	ACH90996	ACH90996 Human gen
C	76	228.6	59.8	518	12	ACH75824	ACH75824 Human gen
C	77	228.4	59.8	524	12	ACH78347	ACH78347 Human gen
C	78	225.2	59.0	572	12	ACH92271	ACH92271 Human gen
C	79	225.2	59.0	885	12	ACH89540	ACH89540 Human gen
C	80	221.2	57.9	533	12	ACH75799	ACH75799 Human gen
C	81	220	57.6	1098	5	AA570933	AA570933 DNA encod
C	82	218.4	57.2	600	12	ADN98428	ADN98428 Novel hum
C	83	218.4	57.2	600	12	ADN99996	ADN99996 Novel hum
C	84	217.2	56.9	566	12	ACH78423	ACH78423 Human gen
C	85	217.2	56.9	327	12	ACH81696	ACH81696 Human gen
C	86	213.6	55.9	580	12	ACH75683	ACH75683 Human gen
C	87	213.4	55.9	566	12	ACH77296	ACH77296 Human gen
C	88	211.4	55.3	532	12	ACH73626	ACH73626 Human gen
C	89	202.6	53.0	308	12	ACH84234	ACH84234 Human gen
C	90	200.8	52.6	343	3	AACT6463	AACT6463 Human ORF
C	91	195.6	51.2	549	12	ACH75813	ACH75813 Human gen
C	92	195.2	51.1	559	6	AB058182	AB058182 Human COI
C	93	183.4	48.0	261	12	ACH84104	ACH84104 Human gen

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 1752.31 Seconds

(without alignments)
10563.118 Million cell updates/sec

Title: US-09-854-867-4

Perfect score: 382

Sequence: 1 ctgcagacactactctccag.....ctgcctccatagatc 382

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database:

GenBank:
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	382	9 HUMREP	M27785 Human D2223
2	377.2	98.7	213227	9 AC138772	AC138772 Homo sapi
3	375.6	98.3	157733	9 AC138771	AC138771 Homo sapi
4	375.6	98.3	155081	2 CR382332	CR382332 Homo sapi
5	375.6	98.3	216075	2 AC138777	AC138777 Homo sapi
6	374	97.9	110000	2 BX511044_0	BX511044 Homo sapi
7	374	97.9	191109	2 AC027456	AC027456 Homo sapi
8	374	97.9	201709	9 BX004987	BX004987 Human DNA
9	370.8	97.1	484	9 HUMSNONA	M76594 Homo sapien
10	367.6	96.2	151418	2 AC025100	AC025100 Homo sapi
11	366	95.8	183261	2 AC148028	AC148028 Homo sapi
12	366	95.8	191469	2 AC145212	AC145212 Homo sapi
13	364.4	95.4	1959	6 CO095136	CO095136 Sequence
14	364.4	95.4	1959	6 CO172418	CO172418 Sequence
15	364.4	95.4	1959	6 CO201588	CO201588 Sequence
16	364.4	95.4	1959	6 CO217119	CO217119 Sequence
17	364.4	95.4	1959	6 CO292793	CO292793 Sequence
18	364.4	95.4	1959	6 CO329774	CO329774 Sequence
19	364.4	95.4	114546	2 HSNAC000382	AC000382 Homo sapi

20	332.4	87.0	110000	2 BX511044_2	BX511044_2
21	332.4	87.0	110898	9 AL355973	AL355973 Human DNA
22	330.8	86.6	152296	9 CR381535	CR381535 Human DNA
23	330.8	86.6	158069	9 CR392039	CR392039 Human DNA
24	330.8	86.6	208765	9 AC118282	AC118282 Homo sapi
25	329.2	86.2	102530	2 AC147050	AC147050 Homo sapi
26	329.2	86.2	136511	2 AC145621	AC145621 Homo sapi
27	329.2	86.2	141075	2 AC026079	AC026079 Homo sapi
28	329.2	86.2	145618	2 AC024235	AC024235 Homo sapi
29	329.2	86.2	152777	2 AC027762	AC027762 Homo sapi
30	329.2	86.2	155655	2 AC140113	AC140113 Homo sapi
31	329.2	86.2	155813	2 AC134878	AC134878 Homo sapi
32	329.2	86.2	167426	2 AC091085	AC091085 Homo sapi
33	329.2	86.2	171176	2 AC119751	AC119751 Homo sapi
34	309.4	81.0	165731	2 BX640538	BX640538 Human DNA
35	309.4	81.0	167647	2 AC148024	AC148024 Homo sapi
36	309.4	81.0	302859	2 AC044785	AC044785 Homo sapi
37	305.8	80.1	66797	2 AC084718	AC084718 Homo sapi
38	305.8	80.1	190724	2 AC078877	AC078877 Homo sapi
39	304.2	79.6	160460	2 AC024374	AC024374 Homo sapi
40	304.2	79.6	161536	2 AC024318	AC024318 Homo sapi
41	304.2	79.6	179693	2 AL591856	AL591856 Human DNA
42	304.2	79.6	192016	2 AC026540	AC026540 Homo sapi
43	288.2	75.4	110000	2 BX511044_3	BX511044_3
44	288.2	75.4	127682	2 AL137861	AL137861 Human DNA
45	288.2	75.4	133948	2 BX322233	BX322233 Homo sapi
46	286.6	75.0	194050	9 AC138774	AC138774 Homo sapi
47	286.6	74.9	86723	9 AF401203	AF401203 Homo sapi
48	286	74.9	161147	9 AL354832	AL354832 Human DNA
49	282.8	74.0	195588	9 AL583842	AL583842 Homo sapi
50	280.6	73.5	129414	2 AC068398	AC068398 Homo sapi
51	279.6	73.2	127105	2 AC011881	AC011881 Homo sapi
52	279.6	73.2	210656	9 AC138775	AC138775 Homo sapi
53	276.4	72.4	160460	2 AC024374	AC024374 Homo sapi
54	276.4	72.4	161536	2 AC024318	AC024318 Homo sapi
55	274.8	71.9	2271	6 AX747556	AX747556 Sequence
56	274.8	71.9	2771	9 AK092459	AK092459 Homo sapi
57	274.8	71.9	155662	2 AC024454	AC024454 Homo sapi
58	274.8	71.9	164562	2 AC027471	AC027471 Homo sapi
59	274.8	71.9	202936	9 AC138776	AC138776 Homo sapi
60	273.2	71.5	3189	9 AF402806	AF402806 Homo sapi
61	273.2	71.5	114080	9 AC133123	AC133123 Homo sapi
62	273.2	71.5	155397	9 AL590523	AL590523 Human DNA
63	273.2	71.5	165333	9 BX546492	BX546492 Human DNA
64	273.2	71.5	186739	9 BX572084	BX572084 Human DNA
65	273.2	71.5	191144	9 AC138773	AC138773 Homo sapi
66	271.6	71.1	40247	2 AC145662	AC145662 Homo sapi
67	271.6	71.1	41343	9 AC145652	AC145652 Homo sapi
68	271.6	71.1	128909	2 CR381653	CR381653 Homo sapi
69	271.6	71.1	175055	9 BX571672	BX571672 Human DNA
70	271.6	71.1	183417	2 AC068832	AC068832 Homo sapi
71	271.6	71.1	192016	2 AC026540	AC026540 Homo sapi
72	270	70.7	57789	2 AC091570	AC091570 Homo sapi
73	270	70.7	129889	9 CR381670	CR381670 Human DNA
74	270	70.7	185235	2 AC012661	AC012661 Homo sapi
75	270	70.7	186661	9 AL592170	AL592170 Human DNA
76	269	70.4	186773	9 AC108724	AC108724 Homo sapi
77	268.6	70.3	155958	2 AC024975	AC024975 Homo sapi
78	268.6	70.3	110000	2 BX511044_4	BX511044_4
79	268.6	70.3	160669	2 AC024975	AC024975 Homo sapi
80	268.4	70.3	190724	2 AC078877	AC078877 Homo sapi
81	267.4	70.0	672	6 AC078877	AC078877 Homo sapi
82	267.4	70.0	672	6 CO182330	CO182330 Sequence
83	267.4	70.0	672	6 CO206724	CO206724 Sequence
84	267.4	70.0	672	6 CO230147	CO230147 Sequence
85	267.4	70.0	672	6 CO305528	CO305528 Sequence
86	267.4	70.0	672	6 CO342524	CO342524 Sequence
87	267	69.9	176111	2 AC067949	AC067949 Homo sapi
88	266.8	69.8	142616	2 AC067789	AC067789 Homo sapi
89	266.8	69.8	142616	2 AC067789	AC067789 Homo sapi
90	266.8	69.8	183417	2 AC068832	AC068832 Homo sapi
91	266.4	69.7	177110	2 AC133042	AC133042 Homo sapi
92	266.2	69.7	174588	9 AC011841	AC011841 Homo sapi

Continuation (3 of 4)
AL355973 Human DNA
CR381535 Human DNA
CR392039 Human DNA
AC118282 Homo sapi
AC147050 Homo sapi
AC145621 Homo sapi
AC026079 Homo sapi
AC024235 Homo sapi
AC027762 Homo sapi
AC140113 Homo sapi
AC134878 Homo sapi
AC091085 Homo sapi
AC119751 Homo sapi
BX640538 Human DNA
AC148024 Homo sapi
AC044785 Homo sapi
AC084718 Homo sapi
AC078877 Homo sapi
AC024374 Homo sapi
AC024318 Homo sapi
AL591856 Human DNA
AC026540 Homo sapi
Continuation (4 of 4)
AL137861 Human DNA
BX322233 Homo sapi
AC138774 Homo sapi
AF401203 Homo sapi
AL354832 Human DNA
AL583842 Homo sapi
AC068398 Homo sapi
AC011881 Homo sapi
AC138775 Homo sapi
AC024374 Homo sapi
AC024318 Homo sapi
AX747556 Sequence
AK092459 Homo sapi
AC024454 Homo sapi
AC027471 Homo sapi
AC138776 Homo sapi
AF402806 Homo sapi
AC133123 Homo sapi
AL590523 Human DNA
BX546492 Human DNA
BX572084 Human DNA
AC138773 Homo sapi
AC145662 Homo sapi
AC145652 Homo sapi
CR381653 Homo sapi
BX571672 Human DNA
AC068832 Homo sapi
AC026540 Homo sapi
AC091570 Homo sapi
CR381670 Human DNA
AC012661 Homo sapi
AL592170 Human DNA
AC108724 Homo sapi
AC024975 Homo sapi
Continuation (5 of 5)
AC023586 Homo sapi
AC078877 Homo sapi
CO182330 Sequence
CO206724 Sequence
CO230147 Sequence
CO305528 Sequence
CO342524 Sequence
AC067949 Homo sapi
AC067789 Homo sapi
AC067789 Homo sapi
AC068832 Homo sapi
AC133042 Homo sapi
AC011841 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 258.177 Seconds

(without alignments)
10025.556 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68
Sequence: 1 gattcagctgagagatgctgc.....aagagttacatcactcgtggt 68

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.6	90.6	173	6	CD164663 M11-0090T
2	61.6	90.6	335	6	AG266749 Homo sapi
3	60.6	89.1	616	8	AQ555124 RPT1-11-3
4	60.6	89.1	943	8	AQ743035 HS_5387_B
5	60.6	88.2	400	8	AQ621521 HS_3030_B
6	60.6	88.2	411	8	AQ016754 CTF-HSP-2
7	60.6	88.2	470	8	AQ0789316 HS_3250_A
8	60.6	88.2	532	8	AQ508622 RPT1-11-3
9	60.6	88.2	536	8	AQ466364 HS_5153_B
10	60.6	88.2	617	1	AA174078 zpi18g12.b
11	60.6	88.2	718	8	AQ897999 HS_3122_B
12	60.6	88.2	777	8	AQ749728 HS_5573_A
13	60.6	88.2	844	8	AQ746068 HS_2277_A
14	60.6	88.2	959	8	AQ747420 HS_5537_A
15	58.4	85.9	116	6	CD086997 MCI-0034T
16	58.4	85.9	248	2	BE045056 hm26e10.x
17	58.4	85.9	319	9	AG265802 Homo sapi
18	58.4	85.9	338	8	AQ275828 CITR1-E1-
19	58.4	85.9	446	8	AQ357456 CITR1-E1-
20	58.4	85.9	476	8	AQ165121 HS_3032_B
21	58.4	85.9	491	8	AQ080166 HS_5037_B
22	58.4	85.9	506	8	AQ149095 HS_3165_A
23	58.4	85.9	518	8	AQ165428 HS_3031_A
24	58.4	85.9	529	8	AQ784754 HS_3249_A

C 25	58.4	85.9	538	8	AQ333667 HS_5013_A
C 26	58.4	85.9	547	8	AQ279387 CITR1-E1-
C 27	58.4	85.9	566	8	AQ260254 CITR1-E1-
C 28	58.4	85.9	567	8	AQ355370 CITR1-E1-
C 29	58.4	85.9	575	8	AQ518554 RPT1-11-1
C 30	58.4	85.9	600	8	AQ263555 CITR1-E1-
C 31	58.4	85.9	840	8	AQ897026 HS_3153_A
C 32	58.4	85.9	853	8	AQ787779 HS_3072_A
C 33	58.4	85.9	1093	8	AF139717 AF139717
C 34	57.4	84.4	343	8	AQ083344 RPT1-11-5
C 35	57.4	84.4	541	8	AQ144422 HS_3084_A
C 36	57	83.8	455	2	AM063430 TN0315_KR
C 37	57	83.8	511	8	AQ482389 RPT1-11-2
C 38	57	83.8	556	8	AQ784087 HS_3250_A
C 39	56.8	83.5	339	9	AG266279 Homo sapi
C 40	56.8	83.5	341	8	AQ028509 CIT-HSP-2
C 41	56.8	83.5	415	8	AQ173952 HS_3204_A
C 42	56.8	83.5	451	1	AQ289438 AU289438
C 43	56.8	83.5	465	8	AQ080519 HS_3141_A
C 44	56.8	83.5	509	8	AQ498992 HS_5154_B
C 45	56.8	83.5	522	8	AQ890999 HS_3251_A
C 46	56.8	83.5	542	8	AQ545641 CITR1-E1-
C 47	56.8	83.5	549	8	AQ554710 RPT1-11-4
C 48	56.8	83.5	557	8	AQ428667 CITR1-E1-
C 49	56.8	83.5	558	8	AQ488499 RPT1-11-2
C 50	56.8	83.5	569	8	AQ679339 HS_3156_A
C 51	56.8	83.5	584	8	AQ387826 RPT1-11-15
C 52	56.8	83.5	599	8	AQ312295 RPT1-11-10
C 53	56.8	83.5	609	8	AQ897013 HS_3153_A
C 54	56.8	83.5	617	8	AQ380528 RPT1-11-16
C 55	56.8	83.5	840	8	AQ098658 HS_3129_B
C 56	56.8	83.5	894	8	AQ098657 HS_3129_B
C 57	56.4	82.9	201	8	AQ583739 RPT1-11-4
C 58	56.4	82.9	344	8	AQ066172 CITR1-E1-
C 59	56.4	82.9	660	8	AQ628361 CITR1-E1-
C 60	55.8	82.1	669	8	AQ112283 RPT1-11-10
C 61	55.4	81.5	283	2	BE009212 CM3-BN016
C 62	55.2	81.2	415	8	AQ453368 HS_5192_A
C 63	55.2	81.2	138	2	AM663292 MR3-SN000
C 64	55.2	81.2	308	2	AM851265 IL3-CT022
C 65	55.2	81.2	308	2	AM851265 IL3-CT022
C 66	55.2	81.2	339	9	AG265952 Homo sapi
C 67	55.2	81.2	345	9	AG265844 Homo sapi
C 68	55.2	81.2	380	8	AQ277886 CITR1-E1-
C 69	55.2	81.2	381	8	AQ0203294 HS_3239_A
C 70	55.2	81.2	391	8	AQ095474 HS_3034_A
C 71	55.2	81.2	410	8	AQ471830 CITR1-E1-
C 72	55.2	81.2	413	8	AQ278058 CITR1-E1-
C 73	55.2	81.2	430	8	AQ211059 HS_3234_B
C 74	55.2	81.2	434	8	AQ260253 CITR1-E1-
C 75	55.2	81.2	469	8	B42961 HS-1056-B2-
C 76	55.2	81.2	517	8	AQ477082 CITR1-E1-
C 77	55.2	81.2	542	8	AQ466370 CITR1-E1-
C 78	55.2	81.2	550	8	AQ088573 HS_5531_B
C 79	55.2	81.2	647	8	AQ392523 CITR1-E1-
C 80	55.2	81.2	658	8	AQ418369 RPT1-11-1
C 81	55.2	81.2	685	8	AQ424085 CITR1-E1-
C 82	55.2	81.2	780	8	AQ089800 HS_3122_B
C 83	55.2	81.2	844	8	AQ746350 HS_2277_A
C 84	55.2	81.2	860	8	AQ781811 HS_3148_A
C 85	55.2	81.2	883	8	AQ39605 HS_5381_B
C 86	54.8	80.6	263	8	AQ266169 CITR1-E1-
C 87	54.8	80.6	397	8	AQ166346 HS_3124_B
C 88	54.8	80.6	580	8	AQ628359 CITR1-E1-
C 89	54.8	80.6	684	8	AQ112508 RPT1-11-10
C 90	54.4	80.0	262	8	AQ096680 HS_3032_B
C 91	53.8	79.1	372	9	AG266378 Homo sapi
C 92	53.8	79.1	547	8	AQ139345 HS_3082_A
C 93	53.6	78.8	135	8	AQ347084 RPT1-11-11
C 94	53.6	78.8	270	8	AQ046487 RPT1-11-3
C 95	53.6	78.8	355	8	AQ054049 RPT1-11-3
C 96	53.6	78.8	423	8	AQ346220 HS_5049_B
C 97	53.6	78.8	446	4	BF948124 CM0-NN115

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 44.3008 Seconds
(without alignments)
9130.760 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68 gacacagcagacagatgctc.....aagagtcacacccggt 68

Sequence: 1 gacacagcagacagatgctc.....aagagtcacacccggt 68

Scoring table: IDENTITY NUC
Gapex 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
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- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
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- 21: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	68	US-09-854-867-3	Sequence 3, Appl1
2	61.6	90.6	473	US-09-864-761-2422	Sequence 2422, Ap
3	60	88.2	467	US-10-027-632-319355	Sequence 319355, Ap
4	60	88.2	467	US-10-027-632-319355	Sequence 319355, Ap
5	60	88.2	593	US-10-027-632-3521	Sequence 3521, Ap
6	60	88.2	593	US-10-027-632-3521	Sequence 3521, Ap
7	60	88.2	630	US-10-027-632-1917	Sequence 1917, Ap
8	60	88.2	630	US-10-027-632-1918	Sequence 1918, Ap
9	60	88.2	630	US-10-027-632-1917	Sequence 1917, Ap
10	60	88.2	630	US-10-027-632-1918	Sequence 1918, Ap
11	60	88.2	672	US-10-027-632-113100	Sequence 113100, Ap

12	60	88.2	672	US-10-027-632-113101	Sequence 113101, Ap
13	60	88.2	672	US-10-027-632-113102	Sequence 113102, Ap
14	60	88.2	672	US-10-027-632-113100	Sequence 113100, Ap
15	60	88.2	672	US-10-027-632-113101	Sequence 113101, Ap
16	60	88.2	672	US-10-027-632-113102	Sequence 113102, Ap
17	59	85.9	506	US-09-864-761-13029	Sequence 13029, A
18	58.4	85.9	657	US-10-027-632-315903	Sequence 315903, Ap
19	58.4	85.9	657	US-10-027-632-315903	Sequence 315903, Ap
20	56.8	83.5	530	US-09-814-353-2271	Sequence 2271, Ap
21	56.8	83.5	530	US-09-814-353-2271	Sequence 2271, Ap
22	56.8	83.5	574	US-09-814-353-8611	Sequence 8611, Ap
23	55.2	81.2	499	US-09-783-590-4181	Sequence 4181, Ap
24	55.2	81.2	858	US-10-027-632-173562	Sequence 173562, Ap
25	55.2	81.2	858	US-10-027-632-173563	Sequence 173563, Ap
26	55.2	81.2	858	US-10-027-632-173562	Sequence 173562, Ap
27	55.2	81.2	858	US-10-027-632-173563	Sequence 173563, Ap
28	52	76.5	184	US-09-738-973-536	Sequence 536, App
29	52	76.5	184	US-09-854-133-536	Sequence 536, App
30	52	76.5	184	US-10-144-649A-536	Sequence 536, App
31	52	76.5	625	US-10-027-632-3250	Sequence 3250, Ap
32	52	76.5	625	US-10-027-632-3251	Sequence 3251, Ap
33	52	76.5	625	US-10-027-632-3250	Sequence 3250, Ap
34	52	76.5	625	US-10-027-632-3251	Sequence 3251, Ap
35	51.6	75.9	605	US-10-027-632-35155	Sequence 35155, A
36	51.6	75.9	605	US-10-027-632-318612	Sequence 318612, A
37	51.6	75.9	605	US-10-027-632-318612	Sequence 318612, A
38	51.6	75.9	605	US-10-027-632-318612	Sequence 318612, A
39	50.4	74.1	1040	US-10-027-632-2571	Sequence 2571, Ap
40	50.4	74.1	1040	US-10-027-632-2572	Sequence 2572, Ap
41	50.4	74.1	1040	US-10-027-632-2573	Sequence 2573, Ap
42	50.4	74.1	1040	US-10-027-632-2574	Sequence 2574, Ap
43	50.4	74.1	1040	US-10-027-632-2571	Sequence 2571, Ap
44	50.4	74.1	1040	US-10-027-632-2572	Sequence 2572, Ap
45	50.4	74.1	1040	US-10-027-632-2573	Sequence 2573, Ap
46	50.4	74.1	1040	US-10-027-632-2574	Sequence 2574, Ap
47	50	73.5	758	US-10-027-632-4438	Sequence 4438, Ap
48	50	73.5	758	US-10-027-632-4438	Sequence 4438, Ap
49	49	72.1	190	US-09-864-761-29592	Sequence 29592, A
50	48.8	71.8	693	US-10-027-632-17960	Sequence 17960, A
51	48.8	71.8	693	US-10-027-632-17961	Sequence 17961, A
52	48.8	71.8	693	US-10-027-632-17962	Sequence 17962, A
53	48.8	71.8	693	US-10-027-632-17960	Sequence 17960, A
54	48.8	71.8	693	US-10-027-632-17961	Sequence 17961, A
55	48.8	71.8	693	US-10-027-632-17962	Sequence 17962, A
56	48	70.6	617	US-10-027-632-6019	Sequence 6019, Ap
57	48	70.6	617	US-10-027-632-6018	Sequence 6018, Ap
58	48	70.6	617	US-10-027-632-6020	Sequence 6020, Ap
59	48	70.6	617	US-10-027-632-6021	Sequence 6021, Ap
60	48	70.6	617	US-10-027-632-6018	Sequence 6018, Ap
61	48	70.6	617	US-10-027-632-6019	Sequence 6019, Ap
62	48	70.6	617	US-10-027-632-6020	Sequence 6020, Ap
63	48	70.6	617	US-10-027-632-6021	Sequence 6021, Ap
64	45.8	67.4	590	US-10-027-632-311425	Sequence 311425, A
65	45.8	67.4	590	US-10-027-632-311425	Sequence 311425, A
66	44.2	65.0	201	US-09-864-761-19153	Sequence 19153, A
67	39	57.4	220	US-09-783-590-4004	Sequence 4004, Ap
68	38	55.9	209	US-10-242-535A-9959	Sequence 9959, Ap
69	38	55.9	209	US-10-085-783A-9959	Sequence 9959, Ap
70	32.2	47.4	568	US-10-027-632-228175	Sequence 228175, Ap
71	32.2	47.4	568	US-10-027-632-228175	Sequence 228175, Ap
72	31	45.6	1104	US-10-027-632-208393	Sequence 208393, Ap
73	31	45.6	1104	US-10-027-632-208393	Sequence 208393, Ap
74	30.6	45.0	703	US-10-027-632-113092	Sequence 113092, Ap
75	29.6	43.5	400	US-10-027-632-113091	Sequence 113091, Ap
76	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
77	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
78	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
79	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
80	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
81	29.6	43.5	635	US-10-027-632-113091	Sequence 113091, Ap
82	29.4	43.2	370	US-10-027-632-271462	Sequence 271462, Ap
83	29.4	43.2	370	US-10-027-632-271462	Sequence 271462, Ap
84	29.4	43.2	608	US-10-027-632-202596	Sequence 202596, Ap

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 12.3906 Seconds
(without alignments)
8979.909 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68

Sequence: 1 gatcagctgagagatatgctc.....aagagttacacactggt 68

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	68	US-09-573-080A-3	Sequence 3, Appl1
2	52	76.5	184	US-09-854-133-536	Sequence 536, App
3	44.2	65.0	356	US-09-513-999C-13463	Sequence 13463, A
4	32.8	48.2	156942	US-09-949-016-12227	Sequence 12227, A
5	32.8	48.2	156950	US-09-949-016-15946	Sequence 15946, A
6	29	42.6	601	US-09-949-016-149536	Sequence 149536, A
7	29	42.6	601	US-09-949-016-149537	Sequence 149537, A
8	29	42.6	601	US-09-949-016-149597	Sequence 149597, A
9	29	42.6	601	US-09-949-016-12227	Sequence 12227, A
10	29	42.6	601	US-09-949-016-15946	Sequence 15946, A
11	28	41.2	56939	US-09-949-016-13613	Sequence 13613, A
12	28	41.2	76281	US-09-949-016-12708	Sequence 12708, A
13	26	38.2	601	US-09-949-016-149602	Sequence 149602, A
14	25.6	37.6	294	US-09-411-977-10	Sequence 10, Appl1
15	25.6	37.6	294	US-10-057-951-10	Sequence 10, Appl1
16	25.6	37.6	50109	US-09-949-016-14112	Sequence 14112, A
17	25	36.8	470	US-09-621-976-10621	Sequence 10621, A
18	25	36.8	1149	US-09-280-116-196	Sequence 196, App
19	25	36.8	2231	US-09-008-271A-24	Sequence 24, Appl1
20	25	36.8	152481	US-09-949-016-12751	Sequence 12751, A
21	25	36.8	152798	US-09-949-016-12775	Sequence 12775, A
22	25	36.8	152822	US-09-949-016-17518	Sequence 17518, A
23	25	36.8	152822	US-09-949-016-17519	Sequence 17519, A
24	24.8	36.5	168174	US-10-071-411A-63	Sequence 63, Appl1
25	24.8	36.5	168273	US-10-071-411A-2	Sequence 2, Appl1
26	24.6	36.2	2418	US-09-245-808-2	Sequence 2, Appl1
27	24.6	36.2	31573	US-09-949-016-16327	Sequence 16327, A

C	28	24.4	35.9	601	4	US-09-949-016-149541	Sequence 149541, A
C	29	24.4	35.9	601	4	US-09-949-016-149598	Sequence 149598, A
C	30	24.2	35.6	478	4	US-09-621-976-1639	Sequence 1639, Ap
C	31	24	35.3	601	4	US-09-949-016-149544	Sequence 149544, A
C	32	23.8	35.0	497	4	US-09-949-016-149545	Sequence 149545, A
C	33	23.8	35.0	601	4	US-09-621-976-1797	Sequence 1797, Ap
C	34	23.8	35.0	601	4	US-09-949-016-65952	Sequence 65952, A
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C	36	23.8	35.0	601	4	US-09-949-016-182290	Sequence 182290, A
C	37	23.8	35.0	1316	4	US-08-956-171E-111	Sequence 111, App
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C	39	23.8	35.0	13222	3	US-08-936-165A-111	Sequence 111, App
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C	41	23.8	35.0	31300	4	US-09-949-016-15967	Sequence 15967, A
C	42	23.8	35.0	235452	4	US-09-949-016-18224	Sequence 18224, A
C	43	23.4	34.4	26049	4	US-09-949-016-16224	Sequence 16224, A
C	44	23.2	34.1	145928	4	US-09-949-016-15444	Sequence 15444, A
C	45	23.2	34.1	1664976	4	US-08-916-471B-1	Sequence 1, Appl1
C	46	23.2	34.1	1664976	4	US-09-692-570-1	Sequence 1, Appl1
C	47	23	33.8	601	4	US-09-949-016-70935	Sequence 70935, A
C	48	23	33.8	795	4	US-09-949-016-184502	Sequence 184502, A
C	49	23	33.8	795	4	US-09-134-000C-1304	Sequence 1304, Ap
C	50	23	33.8	856	3	US-09-171-517B-15	Sequence 15, Appl1
C	51	23	33.8	2040	4	US-09-252-991A-16099	Sequence 16099, A
C	52	23	33.8	2256	4	US-09-252-991A-16502	Sequence 16502, A
C	53	23	33.8	6688	4	US-09-813-451B-12	Sequence 12, Appl1
C	54	23	33.8	12241	3	US-09-948-138-4	Sequence 4, Appl1
C	55	23	33.8	13737	3	US-09-538-414-10	Sequence 10, Appl1
C	56	23	33.8	13737	4	US-10-074-279-10	Sequence 10, Appl1
C	57	23	33.8	14446	4	US-09-810-861B-4	Sequence 4, Appl1
C	58	23	33.8	190078	4	US-09-949-016-1707	Sequence 12707, A
C	59	23	33.8	190078	4	US-09-949-016-17026	Sequence 17026, A
C	60	23	33.8	276687	4	US-09-949-016-1840	Sequence 13840, A
C	61	22.8	33.5	78157	4	US-09-949-016-16466	Sequence 16466, A
C	62	22.8	33.5	78157	4	US-09-949-016-16467	Sequence 16467, A
C	63	22.6	33.2	1372	4	US-09-976-594-869	Sequence 869, App
C	64	22.6	33.2	37269	4	US-09-949-016-16672	Sequence 16672, A
C	65	22.6	33.2	45249	4	US-09-949-016-13228	Sequence 13228, A
C	66	22.6	33.2	87774	4	US-09-949-016-1821	Sequence 1821, A
C	67	22.6	33.2	238815	4	US-09-949-016-16274	Sequence 16274, A
C	68	22.4	32.9	601	4	US-09-949-016-57396	Sequence 57396, A
C	69	22.4	32.9	1925	4	US-09-620-312D-488	Sequence 488, App
C	70	22.4	32.9	3220	4	US-09-949-016-991	Sequence 981, App
C	71	22.4	32.9	49378	4	US-09-949-016-13408	Sequence 13408, A
C	72	22.4	32.9	268449	4	US-09-949-016-17244	Sequence 17244, A
C	73	22.4	32.9	1230025	4	US-09-198-452A-1	Sequence 1, Appl1
C	74	22.4	32.9	1230230	4	US-09-438-185A-1	Sequence 1, Appl1
C	75	22.2	32.6	601	4	US-09-949-016-139932	Sequence 13932, A
C	76	22.2	32.6	607	3	US-09-105-390-10	Sequence 10, Appl1
C	77	22.2	32.6	1949	3	US-09-105-390-2	Sequence 2, Appl1
C	78	22.2	32.6	3336	4	US-09-949-016-4510	Sequence 4510, Ap
C	79	22.2	32.6	4843	3	US-08-986-485-1	Sequence 1, Appl1
C	80	22.2	32.6	25401	4	US-09-949-016-13345	Sequence 13345, A
C	81	22.2	32.6	50062	4	US-09-949-016-13809	Sequence 13809, A
C	82	22.2	32.6	118067	4	US-09-497-855A-32	Sequence 32, Appl1
C	83	22.2	32.6	145812	4	US-09-949-016-15698	Sequence 15698, A
C	84	22.2	32.6	157032	4	US-09-949-016-15502	Sequence 15502, A
C	85	22	32.4	2100	4	US-10-061-942A-9	Sequence 9, Appl1
C	86	22	32.4	25122	4	US-09-949-016-13132	Sequence 16132, A
C	87	22	32.4	109159	4	US-09-949-016-14169	Sequence 14169, A
C	88	22	32.4	109159	4	US-09-949-016-14170	Sequence 14170, A
C	89	21.8	32.1	277	4	US-09-621-976-2180	Sequence 2180, Ap
C	90	21.8	32.1	277	4	US-09-949-016-1227	Sequence 1227, Ap
C	91	21.8	32.1	2823	4	US-09-704-611-4	Sequence 4, Appl1
C	92	21.8	32.1	2892	4	US-09-704-611-3	Sequence 3, Appl1
C	93	21.8	32.1	24979	2	US-08-147-777-3	Sequence 3, Appl1
C	94	21.8	32.1	24979	5	US-08-452-877-3	Sequence 3, Appl1
C	95	21.8	32.1	24979	5	PCT-US93-03995-3	Sequence 3, Appl1
C	96	21.8	32.1	36148	4	US-09-949-016-19669	Sequence 12969, A
C	97	21.8	32.1	94156	4	US-09-949-016-12388	Sequence 12388, A
C	98	21.8	32.1	102406	4	US-09-949-016-14673	Sequence 14673, A
C	99	21.8	32.1	1830121	4	US-09-557-884-1	Sequence 1, Appl1
C	100	21.8	32.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl1

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 40.8212 Seconds
(without alignments)
9861.108 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68

Sequence: 1 gacacgtgcagagatagtc.....aagatracacacccggc 68

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

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12: geneseq2004as:.*
13: geneseq2004bs:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	68	7	AD330970 Human gen
2	61.6	90.6	473	4	AA112501 Probe #24
3	61.6	90.6	473	4	ABA54205 Human foe
4	61.6	90.6	473	4	ABA23956 Probe #24
5	61.6	90.6	473	4	AAK02483 Human bra
6	61.6	90.6	473	6	ABS02375 Human gen
7	59	86.8	506	4	AA141915 Probe #10
8	59	86.8	506	4	AAK10298 Human bra
9	58.4	85.9	134	10	ADP38189 Human ova
10	56.8	83.5	530	5	AD175869 Human ova
11	56.8	83.5	530	5	AD175869 Human ova
12	56.8	83.5	530	5	AD175869 Human ova
13	55.2	81.2	191	10	ADP38189 Human ova
14	55.2	81.2	191	10	ADP38189 Human ova
15	52	76.5	184	4	AAAD3556 Human lun
16	52	76.5	184	4	AAAD3556 Human lun
17	52	76.5	184	10	ADP68844 Human lun
18	49	72.1	190	4	AA154950 Human lun
19	49	72.1	190	4	AAK22946 Human bra
20	48.8	71.8	305	3	AAAS7082 Human col

21	48.8	71.8	305	6	ABT12504
22	48.8	71.8	305	10	ACD91798
23	46	67.6	294	10	ACD91798
24	44.2	65.0	201	4	AA121692
25	44.2	65.0	201	4	ABA66769 Human foe
26	44.2	65.0	201	4	ABA33833 Probe #12
27	44.2	65.0	201	4	AAK15201 Human bra
28	44.2	65.0	201	6	ABS14880 Human gen
29	44.2	65.0	356	3	AAO93388 Human sec
30	34.2	50.3	166	10	ACD93882 Human col
31	33	48.5	165199	6	ABK83460 Human CDN
32	32.8	48.2	849	4	AAH06738 Human CDN
33	31.4	46.2	117	3	AAAS7076 Human col
34	31.4	46.2	117	6	ABT12498
35	31.4	46.2	117	10	ACD91792
36	30.6	45.0	300	2	AAZ14352
37	28.4	41.8	284	4	AA106830 Human rep
38	28.4	41.8	3003	12	ADN06033
39	28.4	41.8	3083	4	AA106831 Human rep
40	28.4	41.8	4132	11	ACN91983
41	28.4	41.8	8191	4	ABK43033
42	28.4	41.8	8191	4	AA106832 Human rep
43	28.4	41.8	8191	9	ADP61189
44	28	41.2	1989	10	ADAS3544
45	28	41.2	2653	10	ADAS35601
46	28	41.2	4418	4	ABK43031
47	28	41.2	4418	9	ADP61187
48	28	41.2	4418	9	ADP61188
49	28	41.2	4418	9	ADP61188
50	27.6	40.6	648	4	AAK80928
51	27.6	40.6	165199	6	ABK83460
52	27	39.7	3144	11	ADN03175
53	26.8	39.4	544	12	ADN12721
54	26.8	39.4	544	12	ACH77096
55	26.6	39.1	481	4	AA113802
56	26.6	39.1	481	4	AA135162
57	26.6	39.1	481	4	ABS28826
58	26.6	39.1	481	5	AA103676
59	26.4	38.8	523	12	ADN12651
60	26.4	38.8	532	12	ADN12817
61	26.4	38.8	798	12	ADN13802
62	26.4	38.8	2213	10	ADAS3461
63	26.4	38.8	2654	10	ADE54426
64	26.4	38.8	4369	12	ADO63952
65	26	38.2	485	4	AAK16175
66	26	38.2	2114	4	AAH16027
67	25.8	37.9	521	5	AD172251
68	25.8	37.9	521	5	AD172251
69	25.8	37.9	521	5	AD172251
70	25.8	37.9	545	6	ABQ56343 Human col
71	25.6	37.6	619	5	AD143780 Human ova
72	25.6	37.6	291	2	AAV99643 Human t-p
73	25.6	37.6	294	4	AAAD03468 Human t-p
74	25.6	37.6	340	4	AAE92291
75	25.6	37.6	100543	6	ABE52816
76	25.6	37.6	128978	8	ABR83459 Human CDN
77	25.6	37.6	128978	8	AAAS4587 Human LIM
78	25.4	37.4	16273	4	AAK06688 Human imm
79	25.4	37.4	16273	4	AAK79625 Human imm
80	25	36.8	230	10	ADD26739 Human acti
81	25	36.8	429	4	AAH09222 Human CDN
82	25	36.8	471	2	AAV89955 EST clone
83	25	36.8	521	9	ACH35570 Human end
84	25	36.8	537	12	ACH71365 Human gen
85	25	36.8	598	6	ABK35701
86	25	36.8	748	6	ABK35158 Human CDN
87	25	36.8	798	4	AAH07861 Human CDN
88	25	36.8	1149	6	ABK30426 Human G-P
89	25	36.8	1340	6	AACT33907 Human sec
90	25	36.8	1345	6	ABQ54369 Human ova
91	25	36.8	1485	5	AAE79250 DNA encod
92	25	36.8	1485	5	AAE64441 DNA encod
93	25	36.8	1485	5	AAE64441 DNA encod

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 311.93 Seconds

(without alignment)
10563.118 Million cell updates/sec

Title: US-09-854-867-3

Perfect score: 68

Sequence: 1 gacacgtcgcagacatgctc.....aagagttacatcacctgggt 68

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_atc:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.4	97.6	144432	2	AF276983 Homo sapi
2	66.4	97.6	163399	2	AC079860 Homo sapi
3	66.4	97.6	186759	9	AL645608 Human DNA
4	66.4	97.6	200491	2	AB107102 Homo sapi
5	66.4	97.6	327883	2	BX571684 Homo sapi
6	64.8	95.3	38986	9	AY546236 Homo sapi
7	64.8	95.3	104026	9	BS000579 Homo sapi
8	64.8	95.3	142000	2	AC141241 Homo sapi
9	64.8	95.3	152654	9	AC134882 Homo sapi
10	64.8	95.3	170856	2	AC068160 Homo sapi
11	64.8	95.3	175868	2	AC147660 Pan trogl
12	64.8	95.3	177480	2	AC146250 Pan trogl
13	64.8	95.3	179013	9	AC022370 Homo sapi
14	64.8	95.3	181432	9	BX649480 Human DNA
15	64.8	95.3	238079	9	AC147656 Human DNA
16	63.8	93.8	172294	9	BX546479 Human DNA
17	63.2	92.9	345	9	AY546202 Pongo pyg
18	63.2	92.9	346	9	AY546211 Pongo pyg
19	63.2	92.9	346	9	AY546211 Pongo pyg

20	63.2	92.9	416	9	AY546215	AY546215 Pongo pyg
21	63.2	92.9	639	9	AF282526	AF282526 Homo sapi
22	63.2	92.9	1445	9	AF270544	AF270544 Homo sapi
23	63.2	92.9	29891	9	AP006330	AP006330 Homo sapi
24	63.2	92.9	31503	9	AP006328	AP006328 Homo sapi
25	63.2	92.9	36971	9	AL732375	AL732375 Human DNA
26	63.2	92.9	39002	2	AL845259	AL845259 Human DNA
27	63.2	92.9	56731	2	AC087706	AC087706 Homo sapi
28	63.2	92.9	104154	9	AC004902	AC004902 Homo sapi
29	63.2	92.9	110773	2	EX005259	EX005259 Homo sapi
30	63.2	92.9	126625	9	AY028079	AY028079 Homo sapi
31	63.2	92.9	137001	9	AP001005	AP001005 Homo sapi
32	63.2	92.9	142000	2	AC141241	AC141241 Homo sapi
33	63.2	92.9	157606	2	AC069172	AC069172 Homo sapi
34	63.2	92.9	168066	9	AC025226	AC025226 Homo sapi
35	63.2	92.9	170856	2	AC068160	AC068160 Homo sapi
36	63.2	92.9	179013	9	AC022370	AC022370 Homo sapi
37	63.2	92.9	181432	9	BX649480	BX649480 Human DNA
38	63.2	92.9	194917	2	AC069343	AC069343 Homo sapi
39	63.2	92.9	194917	2	AC069343	AC069343 Homo sapi
40	63.2	92.9	211173	9	AL671532	AL671532 Human DNA
41	63.2	92.9	220206	2	AC140726	AC140726 Homo sapi
42	63.2	92.9	220897	2	AL954635	AL954635 Homo sapi
43	61.6	90.6	345	9	HUMRSSAUH	HUMRSSAUH
44	61.6	90.6	347	9	AY546206	AY546206 Pongo pyg
45	61.6	90.6	361	9	AY546197	AY546197 Pongo pyg
46	61.6	90.6	361	9	AY546237	AY546237 Homo sapi
47	61.6	90.6	361	9	AY546242	AY546242 Homo sapi
48	61.6	90.6	394	9	HUMRSSAUP	HUMRSSAUP
49	61.6	90.6	473	6	C0066634	C0066634 Sequence
50	61.6	90.6	473	6	C0171026	C0171026 Sequence
51	61.6	90.6	473	6	C0254249	C0254249 Sequence
52	61.6	90.6	473	6	C0281261	C0281261 Sequence
53	61.6	90.6	473	6	C0328380	C0328380 Sequence
54	61.6	90.6	615	9	AY546195	AY546195 Pongo pyg
55	61.6	90.6	635	9	AF282527	AF282527 Homo sapi
56	61.6	90.6	3664	9	HSU74497	U74497 Human chrom
57	61.6	90.6	133461	2	AC025968	AC025968 Homo sapi
58	61.6	90.6	162209	2	AC020702	AC020702 Homo sapi
59	61.6	90.6	172294	9	BX546479	BX546479 Human DNA
60	61.6	90.6	182649	2	AC023033	AC023033 Homo sapi
61	61.6	90.6	183303	9	AC064866	AC064866 Homo sapi
62	61.6	90.6	183495	9	AC129664	AC129664 Homo sapi
63	61.6	90.6	189853	2	AC130423	AC130423 Homo sapi
64	61.6	90.6	193867	2	AC022179	AC022179 Homo sapi
65	61.6	90.6	211173	9	AL671532	AL671532 Human DNA
66	61.6	90.6	296385	2	BX548253	BX548253 Mus muscu
67	60.6	89.1	167135	9	AC137488	AC137488 Homo sapi
68	60.6	88.2	72	9	HUMRSSAUK	M14615 Human Sauja
69	60.6	88.2	345	9	AY546219	AY546219 Pongo pyg
70	60.6	88.2	345	9	AY546223	AY546223 Pongo pyg
71	60.6	88.2	345	9	AY546227	AY546227 Pongo pyg
72	60.6	88.2	345	9	AY546231	AY546231 Pongo pyg
73	60.6	88.2	361	9	AY546241	AY546241 Homo sapi
74	60.6	88.2	429	9	AY546238	AY546238 Homo sapi
75	60.6	88.2	429	9	AY546240	AY546240 Homo sapi
76	60.6	88.2	429	9	AY546243	AY546243 Homo sapi
77	60.6	88.2	429	9	AY546244	AY546244 Homo sapi
78	60.6	88.2	897	9	AF283053	AF283053 Homo sapi
79	60.6	88.2	901	9	AF283054	AF283054 Homo sapi
80	60.6	88.2	901	9	AF283055	AF283055 Homo sapi
81	60.6	88.2	1656	9	AF270545	AF270545 Homo sapi
82	60.6	88.2	65276	2	AC084190	AC084190 Homo sapi
83	60.6	88.2	162209	2	AC020702	AC020702 Homo sapi
84	60.6	88.2	186051	2	BX005324	BX005324 Mus muscu
85	60.6	88.2	189610	2	AC104301	AC104301 Homo sapi
86	60.6	88.2	189653	2	AC130423	AC130423 Homo sapi
87	60.6	88.2	193867	2	AC022179	AC022179 Homo sapi
88	59.8	86.8	506	6	C0101742	C0101742 Sequence
89	59.8	86.8	506	6	C0336195	C0336195 Sequence
90	58.4	85.9	134	6	AX927327	AX927327 Sequence
91	58.4	85.9	134	8	AJ718176	AJ718176 Nicotiana
92	58.4	85.9	429	9	AY546245	AY546245 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 1101.05 Seconds

(without alignments)
10025.556 Million cell updates/sec

Title: US-09-854-867-2

Perfect score: 290

Sequence: 1 ggcgcggcgccggtgctcac.....agacccctgcctcaaaaaa 290

Scoring table: IDENTITY_NDC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243.6	84.0	342	5	BX484854 DKZ26686L
2	243.6	84.0	409	7	CN276487 17006001
3	243.6	84.0	1686	3	CR619941 full-len
4	243.6	84.0	1755	3	CR609780 full-len
5	242	83.4	368	4	BG059314 nah8c05
6	242	83.4	424	8	AQ113643 CIR-HSP-2
7	240.4	82.9	352	2	BF804385 OVA-CT015
8	240.4	82.9	521	2	AM970571 EST382652
9	240.4	82.9	990	4	BM803650 AGENCOURT
10	238.8	82.3	423	5	BM991096 UI-H-DIO-
11	238.8	82.3	447	5	BX489032 DKZ26686L
12	238.8	82.3	454	1	AI634187 tss5a08.x
13	238.8	82.3	475	8	B81985 RPI11-17P6
14	238.8	82.3	514	1	AT754653 c128c08.x
15	238.8	82.3	832	4	BG697217 602660451
16	238.8	82.3	907	4	BG547933 602576037
17	238.8	82.3	361	8	AQ037231 CIR-HSP-2
18	237.8	82.0	337	5	BUS66980 AGENCOURT
19	237.8	82.0	333	2	BF805088 IL5-CT015
20	237.8	82.0	439	1	AV738383 AV738383
21	237.8	82.0	474	1	AI457313 c173a05.x
22	237.8	82.0	490	8	AQ426532 CITBI-E1-
23	237.8	82.0	575	8	AQ587429 CITBI-E1-
24	237.8	82.0	676	9	AG178621 Pan trogl

25	237.4	81.9	521	5	BUS17227 UI-H-DFO-
26	237.4	81.9	580	5	BO053726 AGENCOURT
27	237.4	81.9	598	5	BO017808 UI-H-EDO-
28	237.4	81.9	616	5	BUS17236 UI-H-DFO-
29	237.4	81.9	731	1	AI687343 tp86f08.x
30	237.2	81.8	372	8	AQ163866 HS 3171.A
31	237.2	81.8	390	5	BUS88888 AGENCOURT
32	237.2	81.8	438	7	CR739570 CR739570
33	237.2	81.8	461	1	AA225406 nc24d02.r
34	237.2	81.8	466	2	AM722294 xul7c12.x
35	237.2	81.8	486	2	AM958862 EST371032
36	237.2	81.8	489	6	AQ480399 RPCI-11-2
37	237.2	81.8	523	6	CA439973 UI-H-DIO-
38	237.2	81.8	590	8	AQ421062 RPCI-11-1
39	237.2	81.8	615	5	BUT83874 in10h03.x
40	237.2	81.8	646	1	AL134940 DFX2762C
41	237.2	81.8	705	5	BUS16173 UI-H-DFO-
42	237.2	81.8	731	7	CN307840 170004182
43	237.2	81.8	745	9	AG015273 Homo sapi
44	237.2	81.8	750	9	AG015272 Homo sapi
45	237.2	81.8	866	8	BZ771933 mct82g05
46	237.2	81.8	960	6	CD245816 AGENCOURT
47	237.2	81.7	857	5	BUS70414 AGENCOURT
48	236.2	81.4	539	8	AQ379787 RPCI11-15
49	236.2	81.4	556	5	BM997889 UI-H-DIO-
50	236.2	81.4	666	5	BUS16112 UI-H-DFO-
51	236.2	81.4	763	1	AUI30337 UI30337
52	236.2	81.4	950	6	CD558421 AGENCOURT
53	235.8	81.3	563	1	AUI44540 UI44540
54	235.8	81.3	775	5	BM905333 AGENCOURT
55	235.6	81.2	380	1	AA613624 n018d03.s
56	235.6	81.2	388	2	AM069227 cr41h09.x
57	235.6	81.2	458	1	AT733856 z019c03.y
58	235.6	81.2	480	1	AI635028 UI-E-DWO-
59	235.6	81.2	482	5	BUT35500 UI-E-DWO-
60	235.6	81.2	583	1	AI923451 wn85g04.x
61	235.6	81.2	582	1	BP872816 BP872816
62	235.6	81.2	607	6	CD369014 UI-H-FTI-
63	235.6	81.2	672	4	BUS88435 603386450
64	235.6	81.2	678	8	AQ387027 RPCI11-15
65	235.6	81.2	697	9	AG010078 Homo sapi
66	235.6	81.2	714	9	AG009651 Homo sapi
67	235.6	81.2	735	7	CF146929 UI-HF-CH0
68	235.6	81.2	1111	4	BM466902 AGENCOURT
69	235.6	81.2	1555	3	BC022315 Homo sapi
70	235.6	81.2	2820	3	AF318360 Homo sapi
71	235.6	81.2	5404	3	CR749478 Homo sapi
72	235.6	81.2	5535	3	AI601229 ar88h09.x
73	235.2	81.1	486	1	AQ744206 HS 5508.A
74	235.2	81.1	967	8	BUS40252 AGENCOURT
75	234.8	81.0	333	5	BM983330 UI-CF-DUI
76	234.8	81.0	472	5	BM802793 AGENCOURT
77	234.8	81.0	1100	4	BUS65560 AGENCOURT
78	234.6	80.9	319	5	AA441810 zw62e02.s
79	234.6	80.9	441	1	BM697526 UI-E-DXO-
80	234.6	80.9	546	4	AV761107 AV761107
81	234.6	80.9	567	1	CD704731 EST21258
82	234.6	80.9	611	6	CF146894 UI-HF-CH0
83	234.6	80.9	698	7	CA308268 UI-H-FTI-
84	234.4	80.9	713	6	B91708 CIR-HSP-217
85	234.4	80.8	360	8	AV760915 AV760915
86	234.2	80.8	338	1	CD238756 FNPBRC11
87	234.2	80.8	560	6	AA483606 ne75d02.s
88	234	80.7	327	1	AA570740 n121c07.s
89	234	80.7	397	6	CA434241 UI-H-DIO-
90	234	80.7	337	1	B76341 RPCI11-15B1
91	234	80.7	421	8	AM105346 x047a10.x
92	234	80.7	451	1	AV695478 AV695478
93	234	80.7	451	1	AA904211 od88e02.s
94	234	80.7	509	2	BF916871 IL3-UT011
95	234	80.7	511	1	AV760508 AV760508
96	234	80.7	568	6	CD517289 AGENCOURT
97	234	80.7	568	6	BUS17227 UI-H-DFO-

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 188.93 Seconds

(without alignments)
9130.766 Million cell updates/sec

Title: US-09-854-867-2

Perfect score: 290
Sequence: 1 ggcgcggcggtgcac.....agaccctgcctcaaaaaa 290

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US07_PUB_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUB_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_PUB_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUB_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_PUB_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10_PUB_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUB_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	290	100.0	US-09-854-867-2	Sequence 2, Appl1
2	284.8	98.2	US-10-115-278-1	Sequence 1, Appl1
3	284.8	98.2	US-10-115-278-1	Sequence 1, Appl1
4	259.2	89.4	US-10-115-278-2	Sequence 2, Appl1
5	259.2	89.4	US-10-115-278-2	Sequence 2, Appl1
6	253.8	87.5	US-10-255-434-1	Sequence 1, Appl1
7	251	86.6	US-10-394-485-26	Sequence 26, Appl1
8	248.6	85.7	US-09-964-824A-509	Sequence 509, App
9	248.6	85.7	US-09-964-824A-509	Sequence 1, Appl1
10	247.4	85.3	US-10-255-434-2	Sequence 2, Appl1
11	246.8	85.1	US-10-017-161-2415	Sequence 2415, Ap

12	246.8	85.1	21925	17	US-10-292-798-2055	Sequence 2055, Ap
13	245.2	84.6	46215	19	US-10-741-600-17973	Sequence 17973, A
14	243.6	84.0	60940	17	US-10-052-482-88	Sequence 88, Appl1
15	243.4	83.9	289	14	US-10-115-278-3	Sequence 3, Appl1
16	243.4	83.9	289	18	US-10-762-966-3	Sequence 966, A
17	241.6	83.3	670	13	US-10-027-632-99522	Sequence 99522, A
18	241.6	83.3	670	13	US-10-027-632-99522	Sequence 99522, A
19	241.6	83.3	670	17	US-10-027-632-99522	Sequence 99523, A
20	241.6	83.3	670	17	US-10-027-632-99523	Sequence 99523, A
21	241.4	83.2	98716	19	US-10-741-600-17754	Sequence 17754, A
22	241	83.1	15577	14	US-10-158-160A-8	Sequence 8, Appl1
23	241	83.1	32367	14	US-10-158-160A-14	Sequence 14, Appl1
24	241	83.1	32367	14	US-10-087-192-370	Sequence 370, App
25	241	83.1	32367	14	US-10-087-192-370	Sequence 202, App
26	240.8	83.0	288	16	US-10-052-482-202	Sequence 14, Appl1
27	240.6	83.0	26184	15	US-10-017-161-2043	Sequence 2043, Ap
28	240.6	83.0	26184	17	US-10-292-798-1689	Sequence 1689, Ap
29	240.4	82.9	2490	13	US-10-027-632-102144	Sequence 102144, Sequence 11607,
30	240.4	82.9	2490	13	US-10-027-632-111607	Sequence 11607,
31	240.4	82.9	2490	17	US-10-027-632-102144	Sequence 11607,
32	240.4	82.9	2490	17	US-10-027-632-111607	Sequence 11607,
33	240.4	82.9	10500	16	US-10-312-495-13	Sequence 13, Appl1
34	240.4	82.9	26371	13	US-10-087-192-1450	Sequence 1450, Ap
35	240.4	82.9	30865	17	US-10-451-867A-2	Sequence 2, Appl1
36	240.4	82.9	32249	10	US-09-764-891-5759	Sequence 5759, Ap
37	240.4	82.9	40000	19	US-10-741-600-18015	Sequence 18015, A
38	240.4	82.9	49620	19	US-10-852-630A-233	Sequence 233, App
39	240.4	82.9	64356	17	US-10-240-425-1100	Sequence 1100, App
40	240.4	82.9	73145	13	US-10-087-192-274	Sequence 274, App
41	240.4	82.9	146547	15	US-10-017-128-1	Sequence 1, Appl1
42	240.4	82.9	166181	18	US-10-723-860-1452	Sequence 1452, Ap
43	240.4	82.9	166181	18	US-10-723-860-3281	Sequence 3281, Ap
44	240.4	82.9	174488	13	US-10-087-192-148	Sequence 148, App
45	240.4	82.9	392000	15	US-10-027-983-11	Sequence 11, Appl1
46	240.4	82.9	392000	17	US-10-448-753-11	Sequence 11, Appl1
47	240.4	82.9	465237	9	US-09-933-267A-1	Sequence 1, Appl1
48	240.4	82.9	822900	17	US-10-292-798-1393	Sequence 1393, Ap
49	240	82.8	28933	18	US-10-712-993-6811	Sequence 6811, Ap
50	240	82.8	29346	17	US-10-085-117-52	Sequence 52, Appl1
51	239.4	82.6	6096	14	US-10-012-600B-132	Sequence 132, App
52	239.4	82.6	35478	18	US-10-322-281-478	Sequence 478, App
53	239.4	82.6	108316	17	US-10-292-798-1789	Sequence 1789, App
54	239.4	82.6	108317	15	US-10-017-161-2143	Sequence 2143, Ap
55	239	82.4	281	16	US-10-229-058B-15	Sequence 15, Appl1
56	239	82.4	665	13	US-10-027-632-152872	Sequence 152872, Sequence 152872,
57	239	82.4	665	17	US-10-027-632-152872	Sequence 152872,
58	239	82.4	913	9	US-09-764-877-3830	Sequence 3830, Ap
59	239	82.4	913	17	US-10-242-515-3830	Sequence 3830, Ap
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63	238.8	82.3	590	17	US-10-027-632-93929	Sequence 93929, A
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65	238.8	82.3	2932	15	US-10-225-567A-447	Sequence 447, App
66	238.8	82.3	2932	17	US-10-305-720-1419	Sequence 1419, Ap
67	238.8	82.3	2932	18	US-10-755-889-595	Sequence 595, App
68	238.8	82.3	4045	10	US-09-764-891-8718	Sequence 8718, Ap
69	238.8	82.3	4045	10	US-09-764-891-8719	Sequence 8719, Ap
70	238.8	82.3	16082	19	US-10-741-600-17975	Sequence 17975, A
71	238.8	82.3	23866	19	US-10-741-600-17736	Sequence 17736, A
72	238.8	82.3	23866	19	US-10-087-192-202	Sequence 202, App
73	238.8	82.3	24898	13	US-10-087-192-1528	Sequence 1528, Ap
74	238.8	82.3	27204	13	US-10-087-192-94	Sequence 94, Appl1
75	238.8	82.3	59588	15	US-10-017-161-2233	Sequence 2233, Ap
76	238.8	82.3	59588	17	US-10-292-798-1879	Sequence 1879, Ap
77	238.8	82.3	139359	17	US-10-236-031B-61	Sequence 61, Appl1
78	238.8	82.3	146547	15	US-10-017-128-1	Sequence 1, Appl1
79	238.8	82.3	160711	18	US-10-450-828-86	Sequence 86, Appl1
80	238.8	82.3	160711	18	US-10-723-860-1452	Sequence 1452, Ap
81	238.8	82.3	166181	18	US-10-723-860-3281	Sequence 3281, App
82	238.8	82.3	227931	17	US-10-085-117-274	Sequence 274, App
83	238.8	82.2	580	13	US-10-027-632-133868	Sequence 133868,

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 52.8424 Seconds
(without alignments)
8979.909 Million cell updates/sec

Title: US-09-854-867-2
Perfect score: 290
Sequence: 1 ggcgcggcgccgctgcac.....agaccctcgtcaaaaaa 290

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	290	100.0	290	4	US-09-573-080A-2
2	251	85.6	283	4	US-08-579-445-26
3	249.2	85.9	282	1	US-08-133-629-8
4	245.2	84.6	36756	4	US-09-949-016-12216
5	245.2	84.6	38206	4	US-09-949-016-15527
6	245.2	84.6	63930	4	US-09-949-016-12270
7	245.2	84.6	109690	4	US-09-949-016-13525
8	243.8	84.1	601	4	US-09-949-016-13582
9	243.8	84.1	601	4	US-09-949-016-16101
10	243.8	84.1	601	4	US-09-949-016-16120
11	243.8	84.1	601	4	US-09-949-016-16120
12	243.8	84.0	601	4	US-09-949-016-16120
13	243.6	84.0	601	4	US-09-949-016-16120
14	243.6	84.0	39489	4	US-09-949-016-13866
15	243.6	84.0	70828	4	US-09-949-016-12122
16	243.2	83.9	601	4	US-09-949-016-15491
17	243.2	83.9	601	4	US-09-949-016-15491
18	243.2	83.9	601	4	US-09-949-016-15491
19	243.2	83.9	601	4	US-09-949-016-15491
20	242.6	83.7	25160	4	US-09-949-016-13065
21	242.6	83.7	25162	4	US-09-949-016-13065
22	242.6	83.7	25162	4	US-09-949-016-13065
23	242	83.4	11929	4	US-09-949-016-12597
24	242	83.4	18197	4	US-09-949-016-12597
25	242	83.4	18197	4	US-09-949-016-12597
26	242	83.4	100463	4	US-09-949-016-12511
27	242	83.4	100468	4	US-09-949-016-13725

28	241.6	83.3	601	4	US-09-949-016-67217	Sequence 67217, A
29	241.6	83.3	601	4	US-09-949-016-194228	Sequence 194228, A
30	241	83.1	19237	4	US-09-949-016-13666	Sequence 13666, A
31	241	83.1	29927	4	US-09-949-016-11814	Sequence 11814, A
32	241	83.1	29927	4	US-09-949-016-14747	Sequence 14747, A
33	241	83.1	29927	4	US-09-949-016-17475	Sequence 17475, A
34	241	83.1	37802	4	US-09-949-016-12639	Sequence 12639, A
35	241	83.1	43550	4	US-09-949-016-12400	Sequence 12400, A
36	241	83.1	43555	4	US-09-949-016-13993	Sequence 13993, A
37	240.8	83.0	58014	4	US-09-949-016-17448	Sequence 17448, A
38	240.8	83.0	83597	4	US-09-949-016-16040	Sequence 16040, A
39	240.4	82.9	601	4	US-09-949-016-93065	Sequence 93065, A
40	240.4	82.9	601	4	US-09-949-016-194227	Sequence 194227, A
41	240.4	82.9	10849	4	US-09-949-016-13007	Sequence 13007, A
42	240.4	82.9	18200	4	US-09-949-016-15660	Sequence 15660, A
43	240.4	82.9	18200	4	US-09-949-016-15661	Sequence 15661, A
44	240.4	82.9	19719	4	US-09-949-016-15662	Sequence 15662, A
45	240.4	82.9	24428	4	US-09-949-016-15663	Sequence 15663, A
46	240.4	82.9	24428	4	US-09-949-016-17262	Sequence 17262, A
47	240.4	82.9	24428	4	US-09-949-016-17262	Sequence 17262, A
48	240.4	82.9	41393	4	US-09-949-016-16012	Sequence 16012, A
49	240.4	82.9	47781	4	US-09-949-016-16493	Sequence 16493, A
50	240.4	82.9	47781	4	US-09-949-016-16493	Sequence 16494, A
51	240.4	82.9	126468	4	US-09-949-016-14418	Sequence 14418, A
52	240.4	82.9	131724	4	US-09-949-016-14418	Sequence 14418, A
53	240.4	82.9	227750	4	US-09-949-016-12893	Sequence 12893, A
54	240.4	82.9	227750	4	US-09-949-016-17175	Sequence 17175, A
55	240.4	82.9	392000	4	US-10-027-983-11	Sequence 11, Appl
56	240	82.8	601	4	US-09-949-016-93066	Sequence 93066, A
57	240	82.8	601	4	US-09-949-016-194226	Sequence 194226, A
58	239.4	82.6	678533	4	US-09-949-016-14577	Sequence 14577, A
59	239.4	82.6	678533	4	US-09-949-016-14578	Sequence 14578, A
60	238.8	82.3	601	4	US-09-949-016-59318	Sequence 59318, A
61	238.8	82.3	2932	4	US-09-016-434-1419	Sequence 1419, Ap
62	238.8	82.3	2932	4	US-09-016-434-1419	Sequence 1419, Ap
63	238.8	82.3	2932	4	US-09-016-434-1419	Sequence 1419, Ap
64	238.8	82.3	18264	4	US-09-949-016-13030	Sequence 13030, A
65	238.8	82.3	46381	4	US-09-949-016-13466	Sequence 13466, A
66	238.8	82.3	62846	4	US-09-949-016-12823	Sequence 12823, A
67	238.8	82.3	92074	4	US-09-949-016-17563	Sequence 17563, A
68	238.4	82.2	601	4	US-09-949-016-14231	Sequence 14231, A
69	238.4	82.2	601	4	US-09-949-016-14231	Sequence 14231, A
70	237.8	82.0	29629	3	US-09-729-995-3	Sequence 3, Appl
71	237.8	82.0	29629	3	US-10-135-689-3	Sequence 3, Appl
72	237.8	82.0	29629	3	US-10-135-689-3	Sequence 3, Appl
73	237.8	82.0	29629	3	US-10-135-689-3	Sequence 3, Appl
74	237.6	81.9	11939	4	US-09-949-016-15334	Sequence 15334, A
75	237.2	81.8	601	4	US-09-949-016-13232	Sequence 13232, A
76	237.2	81.8	601	4	US-09-949-016-15458	Sequence 15458, A
77	237.2	81.8	601	4	US-09-949-016-175820	Sequence 175820, A
78	237.2	81.8	9208	4	US-09-949-016-15567	Sequence 15567, A
79	237.2	81.8	11406	4	US-09-949-016-17355	Sequence 17355, A
80	237.2	81.8	13248	4	US-09-949-016-12824	Sequence 12824, A
81	237.2	81.8	13248	4	US-09-949-016-14330	Sequence 14330, A
82	237.2	81.8	14205	4	US-09-949-016-16196	Sequence 16196, A
83	237.2	81.8	14205	4	US-09-949-016-16196	Sequence 16196, A
84	237.2	81.8	17731	4	US-09-949-016-13472	Sequence 13472, A
85	237.2	81.8	22372	4	US-09-949-016-17459	Sequence 17459, A
86	237.2	81.8	23716	4	US-09-949-016-16580	Sequence 16580, A
87	237.2	81.8	24020	4	US-09-949-016-17533	Sequence 17533, A
88	237.2	81.8	33099	4	US-09-949-016-16094	Sequence 16094, A
89	237.2	81.8	34422	4	US-09-949-016-12701	Sequence 12701, A
90	237.2	81.8	34422	4	US-09-949-016-16075	Sequence 16075, A
91	237.2	81.8	36791	4	US-09-949-016-17451	Sequence 17451, A
92	237.2	81.8	41664	4	US-09-536-059-1	Sequence 1, Appl
93	237.2	81.8	53737	4	US-09-949-016-16197	Sequence 16197, A
94	237.2	81.8	57507	4	US-09-949-016-15019	Sequence 15019, A
95	237.2	81.8	63783	4	US-09-949-016-13756	Sequence 13756, A
96	237.2	81.8	94748	4	US-09-949-016-12648	Sequence 12648, A
97	237.2	81.8	94758	4	US-09-949-016-16741	Sequence 16741, A
98	237.2	81.8	96729	4	US-09-949-016-15006	Sequence 15006, A
99	237.2	81.8	100463	4	US-09-949-016-12511	Sequence 12511, A
100	237.2	81.8	100468	4	US-09-949-016-13725	Sequence 13725, A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 174.09 seconds
(without alignments)
9861.108 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	251	86.6	283	12	AD004061
6	249.2	85.9	282	2	AA162346
7	248.6	85.7	291	6	ABL67475
8	248.6	85.7	291	6	ABL67475
9	247.4	85.3	301	10	ADH59596
10	246.8	85.1	475	4	AAK77866
11	246.8	85.1	21925	10	AD87602
12	243.6	84.0	825	4	AAK6384
13	243.6	84.0	1272	4	AAK73756
14	243.6	84.0	1272	4	AAK73757
15	243.6	84.0	1744	6	AB270301
16	243.6	84.0	60940	9	AD802582
17	243.6	84.0	60940	10	AD872320
18	243.6	84.0	60940	10	AD855530
19	242	83.4	127145	13	AD80254
20	241	83.1	15577	2	AAV35616

21	241	83.1	32367	2	AAV35620	AAV35620 Human SHO
22	241	83.1	35236	11	ACN44094	ACN44094 Human gen
23	241	83.1	57502	12	ADQ97092	ADQ97092 Human can
24	241	83.1	59554	9	AD802696	AD802696 Human TK2
25	241	83.1	59554	10	AD872434	AD872434 Human TK2
26	241	83.1	59554	10	AD859544	AD859544 Human TK2
27	240.6	83.0	26184	6	AD872336	AD872336 Human GPC
28	240.4	82.9	10500	6	ABK13086	ABK13086 DNA encod
29	240.4	82.9	22130	4	AAK77045	AAK77045 Human imm
30	240.4	82.9	26371	11	ACN44814	ACN44814 Human gen
31	240.4	82.9	30865	6	ABQ75494	ABQ75494 Human epi
32	240.4	82.9	32249	4	AA103071	AA103071 Human rep
33	240.4	82.9	32249	4	AB197407	AB197407 Human tes
34	240.4	82.9	32249	5	AB15833	AB15833 Human ner
35	240.4	82.9	73145	11	ACN44030	ACN44030 Human gen
36	240.4	82.9	110000	6	ABK90193_1	ABK90193_1 of
37	240.4	82.9	110000	6	ABQ87681_1	ABQ87681_1 of
38	240.4	82.9	110000	6	ABK3717_1	ABK3717_1 of
39	240.4	82.9	110000	10	AD881391_0	AD881391 Partial g
40	240.4	82.9	110000	10	ADG70184_1	ADG70184_1 of
41	240.4	82.9	146547	8	AB280817	AB280817 Human pho
42	240.4	82.9	166181	12	ADQ20461	ADQ20461 Human sof
43	240.4	82.9	166181	12	ADQ18633	ADQ18633 Human sof
44	240.4	82.9	174448	11	ACN43946	ACN43946 Human gen
45	240.4	82.9	238417	13	ABD32868	ABD32868 Human can
46	240.4	82.9	349901	10	AD868940	AD868940 Human GPC
47	240.4	82.9	349938	10	AD87621	AD87621 Human GPC
48	240	82.8	291	4	AA541852	AA541852 Genomic s
49	240	82.8	291	4	AA541901	AA541901 Genomic s
50	240	82.8	291	4	AA541804	AA541804 Genomic s
51	240	82.8	291	4	AAK85532	AAK85532 Human imm
52	240	82.8	291	4	AAK69652	AAK69652 Human imm
53	240	82.8	291	4	AAK85482	AAK85482 Human imm
54	239.4	82.6	6096	6	ABK92513	ABK92513 Human pro
55	239.4	82.6	35478	13	ABD33376	ABD33376 Human can
56	239.4	82.6	108316	10	AD87336	AD87336 Human GPC
57	239	82.4	913	4	AA137465	AA137465 Human mus
58	239	82.4	913	12	AD131203	AD131203 CDNA enco
59	239	82.4	913	12	AD131203	AD131203 Human mus
60	238.8	82.3	1413	3	AD00684	AD00684 Human Hyd
61	238.8	82.3	1920	10	AD452630	AD452630 Human cod
62	238.8	82.3	2218	12	AD064132	AD064132 Novel hum
63	238.8	82.3	2227	10	AD181515	AD181515 Human pro
64	238.8	82.3	2502	13	AD867013	AD867013 Human can
65	238.8	82.3	2532	2	AA025388	AA025388 TXA2 rece
66	238.8	82.3	2532	2	AA32161	AA32161 Human thr
67	238.8	82.3	2932	2	AA232162	AA232162 Human end
68	238.8	82.3	2932	5	AA658879	AA658879 DNA encod
69	238.8	82.3	2932	6	ABK83654	ABK83654 Human CDN
70	238.8	82.3	2932	8	AB242829	AB242829 Human thr
71	238.8	82.3	2932	10	ADG32934	ADG32934 Human DNA
72	238.8	82.3	2932	12	ACAS6821	ACAS6821 Human sig
73	238.8	82.3	2932	12	AD156617	AD156617 Human pol
74	238.8	82.3	2932	12	AD030052	AD030052 Human GPC
75	238.8	82.3	2932	13	ADRI4594	ADRI4594 Human NF-
76	238.8	82.3	2932	13	ADP56011	ADP56011 Human PRO
77	238.8	82.3	4045	4	AA106031	AA106031 Human rep
78	238.8	82.3	4045	4	AA106030	AA106030 Human rep
79	238.8	82.3	4045	4	AB198596	AB198596 Human tes
80	238.8	82.3	4045	4	AB198595	AB198595 Human tes
81	238.8	82.3	7818	4	AAK51950	AAK51950 Human pol
82	238.8	82.3	20733	9	AA058742	AA058742 Human tra
83	238.8	82.3	24898	11	ACN43982	ACN43982 Human gen
84	238.8	82.3	27204	11	ACN44866	ACN44866 Human gen
85	238.8	82.3	32229	13	AD67012	AD67012 Human can
86	238.8	82.3	47882	11	ACN43910	ACN43910 Human gen
87	238.8	82.3	59588	10	AD87426	AD87426 Human GPC
88	238.8	82.3	139389	6	ABK84795	ABK84795 Human CDN
89	238.8	82.3	139389	9	ABD70369	ABD70369 PAC 6802
90	238.8	82.3	139389	12	ADU37148	ADU37148 Human mal
91	238.8	82.3	146547	8	AB280817	AB280817 Human pho
92	238.8	82.3	160771	6	AB088179	AB088179 Human ost
93	238.8	82.3	166181	12	ADQ20461	ADQ20461 Human sof

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 1330.29 Seconds

(without alignments)
10563.118 Million cell updates/sec

Title: US-09-854-867-2

Perfect score: 290

Sequence: 1 ggcgcggcgccgctgcac.....agaccctgcctcaaaaaa 290

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : GenBank1:
1: gb_ba:
2: gb_hcg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pac:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_scs:
12: gb_sy:
13: gb_un:
14: gb_vl:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	290	12 HSU14567	U14567 ***ALU WARM
2	256.4	88.4	37680	2 AL359985	AL359985 Homo sapi
3	254.8	87.9	321519	2 AL714004	AL714004 Homo sapi
4	253.8	87.5	301	6 AX741027	AX741027 Sequence
5	253.2	87.3	110000	2 AL831785_2	Continuation (3) of
6	251.4	86.7	321519	2 AL714004	AL714004 Homo sapi
7	251	86.6	283	6 AR322101	AR322101 Sequence
8	250	86.2	686	11 AF003745	AF003745 Human chr
9	250	86.2	110000	2 AL831785_4	Continuation (5) of
10	249.2	85.9	282	6 I34294	I34294 Sequence 8
11	248.6	85.7	281	6 AX335303	AX335303 Sequence
12	248.6	85.7	281	6 AX337621	AX337621 Sequence
13	248.6	85.7	281	12 HSU14573	U14573 ***ALU WARM
14	248.4	85.7	83885	2 AC074301	AC074301 Homo sapi
15	248.4	85.7	195986	2 AC116933	AC116933 Papio anu
16	248.4	85.7	223879	9 AC008735	AC008735 Homo sapi
17	248.4	85.7	235286	9 AC136285	AC136285 Homo sapi
18	247.4	85.3	301	6 AX741028	AX741028 Sequence
19	247.4	85.3	940	9 AY181054	AY181054 Pongo pyg

20	247.4	85.3	74486	9 AC055764	AC055764 Homo sapi
21	247.4	85.3	167110	2 AC022621	AC022621 Homo sapi
22	247.4	85.3	172558	9 AC023509	AC023509 Homo sapi
23	246.8	85.1	21925	6 AX647863	AX647863 Sequence
24	246.8	85.1	37959	9 AC011551	AC011551 Homo sapi
25	246.8	85.1	69004	9 AL355145	AL355145 Homo sapi
26	246.8	85.1	69113	9 AL359960	AL359960 Homo sapi
27	246.8	85.1	148624	2 AC084815	AC084815 Homo sapi
28	246.8	85.1	165191	9 HSDJ140A9	HSDJ140A9
29	246.8	85.1	171309	9 AC012146	AC012146 Homo sapi
30	246.8	85.1	173522	2 AC073364	AC073364 Homo sapi
31	246.8	85.1	184621	2 AC104636	AC104636 Homo sapi
32	246.8	85.1	257967	2 AL365337	AL365337 Mus muscu
33	245.8	84.8	81831	9 AL365506	AL365506 Homo sapi
34	245.8	84.8	115296	2 AC084086	AC084086 Homo sapi
35	245.8	84.8	128444	2 AF214634	AF214634 Homo sapi
36	245.8	84.8	168042	2 AC025931	AC025931 Homo sapi
37	245.8	84.8	181047	2 AC016765	AC016765 Homo sapi
38	245.8	84.8	198599	9 AC108448	AC108448 Homo sapi
39	245.8	84.8	221054	2 AC009882	AC009882 Homo sapi
40	245.2	84.6	56330	2 AL353694_3	AL353694_3
41	245.2	84.6	86560	9 AC090505	AC090505 Homo sapi
42	245.2	84.6	120084	9 AC006205	AC006205 Homo sapi
43	245.2	84.6	128829	9 AC127002	AC127002 Homo sapi
44	245.2	84.6	129277	2 AC143642	AC143642 Macaca mu
45	245.2	84.6	141442	9 AC108471	AC108471 Homo sapi
46	245.2	84.6	146350	9 HS225L15	HS225L15
47	245.2	84.6	152154	2 AC136369	AC136369 Homo sapi
48	245.2	84.6	157251	2 AC131311	AC131311 Homo sapi
49	245.2	84.6	161651	9 HS233K16	HS233K16
50	245.2	84.6	174231	9 AC021054	AC021054 Homo sapi
51	245.2	84.6	176438	2 AC126761	AC126761 Homo sapi
52	245.2	84.6	180852	2 AC126765	AC126765 Homo sapi
53	245.2	84.6	201508	2 AC026290	AC026290 Homo sapi
54	245.2	84.6	209157	9 CNS01DW4	CNS01DW4
55	245.2	84.6	209242	9 CNS01DRH	CNS01DRH
56	245.2	84.6	340000	9 HS21C100	HS21C100
57	244.2	84.2	2096	9 HSA343033	HSA343033
58	244.2	84.2	128328	9 AC005839	AC005839
59	244.2	84.2	146358	9 HS3D11	HS3D11
60	244.2	84.2	155731	9 AP001205	AP001205 Homo sapi
61	244.2	84.2	174185	2 AC116930	AC116930 Homo sapi
62	244.2	84.2	174185	2 AC034158	AC034158 Homo sapi
63	243.6	84.0	25803	9 AC096510	AC096510 Homo sapi
64	243.6	84.0	40602	9 HSE140F8	HSE140F8
65	243.6	84.0	41159	9 AC004755	AC004755 Homo sapi
66	243.6	84.0	60940	6 AX695473	AX695473 Sequence
67	243.6	84.0	72800	9 AL354757	AL354757 Human DNA
68	243.6	84.0	73463	9 HSB7890015	HSB7890015
69	243.6	84.0	74549	9 AL161785	AL161785 Human DNA
70	243.6	84.0	103694	2 AL162262	AL162262 Homo sapi
71	243.6	84.0	103694	2 AC004836	AC004836 Homo sapi
72	243.6	84.0	140489	2 AC023066	AC023066 Homo sapi
73	243.6	84.0	142591	2 AC092507	AC092507 Homo sapi
74	243.6	84.0	142591	2 AL589843	AL589843 Human DNA
75	243.6	84.0	142726	9 AC104836	AC104836 Homo sapi
76	243.6	84.0	145736	2 AL451139	AL451139 Human DNA
77	243.6	84.0	151624	2 AC072054	AC072054 Mus muscu
78	243.6	84.0	154037	2 AL713970	AL713970 Homo sapi
79	243.6	84.0	158341	2 AL162496	AL162496 Homo sapi
80	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
81	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
82	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
83	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
84	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
85	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
86	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
87	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
88	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
89	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
90	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
91	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi
92	243.6	84.0	162165	2 AL162496	AL162496 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:09:22 ; Search time 649.24 Seconds

(without alignments)
10025.556 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171
Sequence: 1 aattctcagtaactctctcgtg.....ctatagaactagacagcaat 171

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	259	8	AQ106174 HS_3055_A
2	171	100.0	352	8	AQ106174 HS_3055_A
3	171	100.0	359	8	AQ103653 HS_3093_A
4	171	100.0	371	8	AQ103653 HS_3093_A
5	171	100.0	373	8	AQ103653 HS_3093_A
6	171	100.0	389	8	AQ103653 HS_3093_A
7	171	100.0	389	8	AQ103653 HS_3093_A
8	171	100.0	396	8	AQ103653 HS_3093_A
9	171	100.0	398	8	AQ103653 HS_3093_A
10	171	100.0	409	8	AQ103653 HS_3093_A
11	171	100.0	414	2	AM238038 XP13H01.X
12	171	100.0	424	8	AQ090237 HS_3007_B
13	171	100.0	429	8	AQ090237 HS_3007_B
14	171	100.0	435	8	AQ090237 HS_3007_B
15	171	100.0	440	8	AQ090237 HS_3007_B
16	171	100.0	447	8	AQ090237 HS_3007_B
17	171	100.0	457	8	AQ090237 HS_3007_B
18	171	100.0	468	8	AQ090237 HS_3007_B
19	171	100.0	485	8	AQ090237 HS_3007_B
20	171	100.0	485	8	AQ090237 HS_3007_B
21	171	100.0	487	8	AQ090237 HS_3007_B
22	171	100.0	503	8	AQ090237 HS_3007_B
23	171	100.0	504	8	AQ090237 HS_3007_B
24	171	100.0	505	8	AQ090237 HS_3007_B

25	171	100.0	517	8	AQ627376 CITBI-EI-
26	171	100.0	524	8	AQ311157 CITBI-EI-
27	171	100.0	539	8	AQ544562 CITBI-EI-
28	171	100.0	557	8	AQ587898 CITBI-EI-
29	171	100.0	562	8	AQ628044 CITBI-EI-
30	171	100.0	575	8	AQ778027 HS_3119_A
31	171	100.0	586	8	AQ625435 CITBI-EI-
32	171	100.0	594	8	AQ626137 CITBI-EI-
33	171	100.0	608	8	AQ428825 CITBI-EI-
34	171	100.0	611	8	AQ626151 CITBI-EI-
35	171	100.0	636	8	AQ394830 CITBI-EI-
36	171	100.0	638	8	AQ545889 CITBI-EI-
37	171	100.0	694	8	AQ263099 CITBI-EI-
38	171	100.0	705	8	AQ624705 CITBI-EI-
39	171	100.0	710	8	AQ695914 HS_3143_B
40	171	100.0	716	8	AQ690829 HS_3100_A
41	171	100.0	744	8	AQ697892 HS_3135_A
42	171	100.0	752	7	CF597202 AGENCOURT
43	171	100.0	770	8	AQ6979157 HS_3184_B
44	171	100.0	776	8	AQ696724 HS_3144_A
45	171	100.0	823	8	AQ694357 HS_3133_A
46	171	100.0	844	8	AQ780798 HS_3104_B
47	170	99.4	436	8	AQ141211 HS_3147_B
48	170	99.4	541	8	AQ118976 HS_3002_A
49	170	99.4	562	8	AQ628431 CITBI-EI-
50	169.4	99.1	272	8	AQ096854 HS_3040_A
51	169.4	99.1	276	8	AQ096829 HS_3056_A
52	169.4	99.1	281	8	AQ545270 CITBI-EI-
53	169.4	99.1	373	8	AQ276733 CITBI-EI-
54	169.4	99.1	380	8	AQ120800 HS_3076_A
55	169.4	99.1	382	8	AQ070064 HS_3027_B
56	169.4	99.1	383	8	AQ151895 HS_3104_A
57	169.4	99.1	385	8	AQ132811 HS_3078_A
58	169.4	99.1	391	8	AQ100468 HS_3061_A
59	169.4	99.1	404	8	AQ627317 CITBI-EI-
60	169.4	99.1	405	8	AQ147619 HS_3067_B
61	169.4	99.1	417	8	AQ094572 HS_3026_B
62	169.4	99.1	420	8	AQ787454 HS_3224_B
63	169.4	99.1	438	8	AQ391364 CITBI-EI-
64	169.4	99.1	439	8	AQ180092 HS_3204_B
65	169.4	99.1	439	8	AQ544561 CITBI-EI-
66	169.4	99.1	464	8	AQ140268 HS_3113_A
67	169.4	99.1	473	8	AQ626094 CITBI-EI-
68	169.4	99.1	487	8	AQ476800 CITBI-EI-
69	169.4	99.1	490	8	AQ625170 CITBI-EI-
70	169.4	99.1	492	8	AQ496965 HS_3044_B
71	169.4	99.1	516	8	AQ209617 HS_3236_A
72	169.4	99.1	519	8	AQ080471 HS_3094_A
73	169.4	99.1	524	8	AQ164360 HS_3001_B
74	169.4	99.1	535	8	AQ130280 HS_3011_B
75	169.4	99.1	535	8	AQ169502 HS_3168_B
76	169.4	99.1	548	8	AQ472497 CITBI-EI-
77	169.4	99.1	551	8	AQ475110 CITBI-EI-
78	169.4	99.1	569	8	AQ355720 CITBI-EI-
79	169.4	99.1	579	8	AQ628705 RPCI-11-4
80	169.4	99.1	581	8	AQ628461 CITBI-EI-
81	169.4	99.1	591	8	AQ390810 CITBI-EI-
82	169.4	99.1	600	8	AQ260970 CITBI-EI-
83	169.4	99.1	635	8	AQ626188 CITBI-EI-
84	169.4	99.1	643	8	AQ392767 CITBI-EI-
85	169.4	99.1	650	8	AQ393824 CITBI-EI-
86	169.4	99.1	652	8	AQ624919 CITBI-EI-
87	169.4	99.1	656	8	AQ624919 CITBI-EI-
88	169.4	99.1	659	8	AQ781152 HS_3104_A
89	169.4	99.1	694	8	AQ309599 CITBI-EI-
90	169.4	99.1	694	8	AQ392954 CITBI-EI-
91	169.4	99.1	695	8	AQ625480 CITBI-EI-
92	169.4	99.1	706	8	AQ425409 CITBI-EI-
93	169.4	99.1	713	8	AQ781731 HS_3122_A
94	169.4	99.1	751	8	AQ697766 HS_3122_A
95	169.4	99.1	758	8	AQ695415 HS_3148_B
96	169.4	99.1	813	8	AQ780847 HS_3113_B
97	169.4	99.1	824	8	AQ781451 HS_3117_A

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 12:45:59 ; Search time 111.403 Seconds
(without alignments)
9130.760 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171

Sequence: 1 aactccagactctctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*

14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*

15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*

20: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*

21: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*

22: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	171	10	US-09-854-867-1
2	161.4	94.4	348	9	US-09-810-935-85
3	161.4	94.4	348	9	US-09-429-755-85
4	161.4	94.4	348	9	US-09-924-400-85
5	161.4	94.4	348	15	US-10-212-679-85
6	150.2	87.8	824	17	US-10-079-137B-85
7	150.2	87.8	824	17	US-10-188-832-33
8	150.2	87.8	824	18	US-10-723-860-6919
9	150.2	87.8	824	18	US-10-723-860-8393
10	147	86.0	570	17	US-10-188-832-52
11	145.4	85.0	458	18	US-10-723-860-2854

12	145.4	85.0	458	18	US-10-723-860-4596	Sequence 4596, Ap
13	145.4	85.0	570	18	US-10-723-860-8316	Sequence 8316, Ap
14	139	81.3	464	18	US-10-723-860-4510	Sequence 4510, Ap
15	131.6	77.0	712	10	US-09-852-386-21	Sequence 21, Appl
16	131.4	76.8	293	9	US-09-810-936-86	Sequence 86, Appl
17	131.4	76.8	293	9	US-09-429-755-86	Sequence 86, Appl
18	131.4	76.8	293	9	US-09-924-400-86	Sequence 86, Appl
19	131.4	76.8	293	15	US-10-212-679-86	Sequence 86, Appl
20	131.4	76.8	293	17	US-10-079-137B-86	Sequence 86, Appl
21	121.4	71.0	674	13	US-10-027-632-228542	Sequence 228542, Ap
22	121.4	71.0	674	17	US-10-027-632-228542	Sequence 228542, Ap
23	118.8	69.5	611	13	US-10-027-632-235501	Sequence 235501, Ap
24	118.8	69.5	611	13	US-10-027-632-235502	Sequence 235502, Ap
25	118.8	69.5	611	13	US-10-027-632-235503	Sequence 235503, Ap
26	118.8	69.5	611	13	US-10-027-632-235504	Sequence 235504, Ap
27	118.8	69.5	611	13	US-10-027-632-235505	Sequence 235505, Ap
28	118.8	69.5	611	17	US-10-027-632-235501	Sequence 235501, Ap
29	118.8	69.5	611	17	US-10-027-632-235502	Sequence 235502, Ap
30	118.8	69.5	611	17	US-10-027-632-235503	Sequence 235503, Ap
31	118.8	69.5	611	17	US-10-027-632-235504	Sequence 235504, Ap
32	118.8	69.5	611	17	US-10-027-632-235505	Sequence 235505, Ap
33	117.8	68.9	784	13	US-10-027-632-325163	Sequence 325163, Ap
34	117.8	68.9	784	17	US-10-027-632-325163	Sequence 325163, Ap
35	116.2	68.0	312477	18	US-10-317-883A-12	Sequence 12, Appl
36	114.6	67.0	689	13	US-10-027-632-248758	Sequence 248758, Ap
37	114.6	67.0	689	17	US-10-027-632-248758	Sequence 248758, Ap
38	114.6	67.0	693	16	US-10-029-386-20307	Sequence 20307, A
39	113	66.1	549	9	US-09-864-761-13107	Sequence 13107, A
40	113	66.1	589	13	US-10-027-632-235484	Sequence 235484, Ap
41	113	66.1	589	13	US-10-027-632-235485	Sequence 235485, Ap
42	113	66.1	589	17	US-10-027-632-235484	Sequence 235484, Ap
43	113	66.1	589	17	US-10-027-632-235485	Sequence 235485, Ap
44	113	66.1	604	13	US-10-027-632-215338	Sequence 215338, Ap
45	113	66.1	604	17	US-10-027-632-215338	Sequence 215338, Ap
46	112.6	65.8	624	13	US-10-027-632-203867	Sequence 203867, Ap
47	112.6	65.8	624	13	US-10-027-632-203868	Sequence 203868, Ap
48	112.6	65.8	624	17	US-10-027-632-203867	Sequence 203867, Ap
49	112.6	65.8	624	17	US-10-027-632-203868	Sequence 203868, Ap
50	111.4	65.1	534	10	US-09-918-995-4123	Sequence 4123, Ap
51	111.4	65.1	600	13	US-10-027-632-232439	Sequence 232439, Ap
52	111.4	65.1	600	13	US-10-027-632-232440	Sequence 232440, Ap
53	111.4	65.1	600	13	US-10-027-632-232441	Sequence 232441, Ap
54	111.4	65.1	600	17	US-10-027-632-232439	Sequence 232439, Ap
55	111.4	65.1	600	17	US-10-027-632-232440	Sequence 232440, Ap
56	111.4	65.1	600	17	US-10-027-632-232441	Sequence 232441, Ap
57	111.4	65.1	607	13	US-10-027-632-207009	Sequence 207009, Ap
58	111.4	65.1	607	17	US-10-027-632-207009	Sequence 207009, Ap
59	111.4	65.1	827	17	US-10-012-697-760	Sequence 760, Ap
60	111.4	65.1	1080	17	US-10-012-697-1269	Sequence 1269, Ap
61	110.8	64.8	340	9	US-09-738-973-552	Sequence 552, App
62	110.8	64.8	340	9	US-09-854-133-552	Sequence 552, App
63	110.8	64.8	340	15	US-10-144-649A-552	Sequence 552, App
64	110.8	64.8	445	13	US-10-027-632-183691	Sequence 183691, Ap
65	110.8	64.8	445	17	US-10-027-632-183691	Sequence 183691, Ap
66	110.2	64.4	515	13	US-10-027-632-92142	Sequence 92142, A
67	110.2	64.4	515	17	US-10-027-632-92142	Sequence 92142, A
68	109.8	64.2	586	13	US-10-027-632-185003	Sequence 185003, Ap
69	109.8	64.2	586	13	US-10-027-632-185004	Sequence 185004, Ap
70	109.8	64.2	586	13	US-10-027-632-185005	Sequence 185005, Ap
71	109.8	64.2	586	17	US-10-027-632-185003	Sequence 185003, Ap
72	109.8	64.2	586	17	US-10-027-632-185004	Sequence 185004, Ap
73	109.8	64.2	586	17	US-10-027-632-185005	Sequence 185005, Ap
74	109.8	64.2	637	13	US-10-027-632-218912	Sequence 218912, Ap
75	109.8	64.2	637	17	US-10-027-632-218912	Sequence 218912, Ap
76	109.8	64.2	1052	13	US-10-027-632-324151	Sequence 324151, Ap
77	109.8	64.2	1052	17	US-10-027-632-324151	Sequence 324151, Ap
78	109.8	64.2	2847	18	US-10-474-070-2	Sequence 2, Appl
79	109.8	64.2	2847	18	US-10-474-070-2	Sequence 2, Appl
80	108.2	63.3	405	10	US-09-918-995-1447	Sequence 3447, Ap
81	108.2	63.3	546	9	US-09-864-761-13071	Sequence 13071, A
82	108.2	63.3	1741	18	US-10-723-860-87	Sequence 87, Appl
83	108.2	63.3	1741	18	US-10-723-860-847	Sequence 847, Ap
84	108.2	63.3	1868	9	US-09-745-600-2	Sequence 2, Appl

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 03:28:42 ; Search time 31.1588 Seconds

(without alignments)
8979.909 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171
Sequence: 1 aattccgaactactctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
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5: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	171	4	US-09-573-080A-1
2	161.4	94.4	348	3	US-08-991-789A-85
3	161.4	94.4	348	3	US-09-062-451-85
4	161.4	94.4	348	3	US-09-598-326-85
5	161.4	94.4	348	4	US-09-289-198-85
6	161.4	94.4	348	4	US-09-429-755-85
7	161.4	94.4	348	4	US-09-699-295-85
8	131.4	76.8	293	3	US-08-991-789A-86
9	131.4	76.8	293	3	US-09-062-451-86
10	131.4	76.8	293	3	US-09-598-326-86
11	131.4	76.8	293	4	US-09-289-198-86
12	131.4	76.8	293	4	US-09-429-755-86
13	131.4	76.8	293	4	US-09-699-295-86
14	112.6	65.8	351	4	US-09-513-999C-34318
15	111.4	65.1	360	4	US-09-513-999C-20597
16	110.8	64.8	340	4	US-09-554-133-552
17	108.2	63.3	1868	4	US-09-554-028-2
18	108.2	62.9	171	1	US-07-858-124-20
19	107.6	62.3	171	1	US-09-949-016-12199
20	106.6	62.3	109038	4	US-09-513-999C-32817
21	104.6	60.9	319	4	US-09-513-999C-32817
22	101.8	59.5	339	3	US-09-554-028-4
23	101.8	59.5	339	3	US-09-554-028-5
24	101.8	59.5	339	3	US-09-745-600-4
25	101.8	59.5	339	4	US-09-745-600-5
26	101.2	59.2	171	1	US-07-858-124-22
27	101	59.1	161	1	US-07-858-124-16

28	101	59.1	1044	3	US-08-695-191-2	Sequence 2, Appl
29	101	59.1	1044	3	US-08-682-080-2	Sequence 2, Appl
30	101	59.1	1044	3	US-09-096-648-2	Sequence 2, Appl
31	99	57.9	197	1	US-07-858-124-18	Sequence 18, Appl
32	97.4	57.0	223	4	US-09-513-999C-22522	Sequence 22522, A
33	97.4	57.0	197	1	US-07-858-124-17	Sequence 17, Appl
34	93.4	54.6	338	3	US-09-254-028-7	Sequence 7, Appl
35	93.4	54.6	338	3	US-09-745-600-7	Sequence 7, Appl
36	92.8	54.3	601	4	US-09-949-016-161507	Sequence 161507, A
37	92.8	54.3	240157	4	US-09-513-999C-16264	Sequence 16264, A
38	91.6	53.6	507	4	US-09-513-999C-22100	Sequence 22100, A
39	91.4	53.5	338	3	US-09-254-028-3	Sequence 3, Appl
40	91.4	53.5	338	3	US-09-745-600-3	Sequence 3, Appl
41	87.6	51.2	340	3	US-09-554-028-6	Sequence 6, Appl
42	87.6	51.2	340	4	US-09-745-600-6	Sequence 6, Appl
43	82.6	48.3	343	3	US-09-643-597-142	Sequence 142, App
44	82.6	48.3	343	4	US-09-480-884A-142	Sequence 142, App
45	82.6	48.3	343	4	US-09-542-615A-142	Sequence 142, App
46	82.6	48.3	343	4	US-09-606-421B-142	Sequence 142, App
47	82.6	48.3	343	4	US-09-921-107-142	Sequence 142, App
48	82.6	48.3	343	4	US-09-466-396A-142	Sequence 142, App
49	82.6	48.3	343	4	US-09-476-496A-142	Sequence 142, App
50	82.6	48.3	343	4	US-09-630-940B-142	Sequence 142, App
51	81.6	47.7	343	4	US-09-285-479-142	Sequence 142, App
52	81.6	47.7	130	1	US-07-938-084-4	Sequence 4, Appl
53	79.2	46.3	186	4	US-09-513-999C-14727	Sequence 14727, A
54	76.8	44.9	273	4	US-09-513-999C-35464	Sequence 35464, A
55	72.8	42.6	131	1	US-07-938-084-5	Sequence 5, Appl
56	71.6	41.9	131	1	US-09-513-999C-20755	Sequence 20755, A
57	67.4	39.4	858	3	US-09-333-521-2	Sequence 2, Appl
58	67.4	39.4	858	4	US-09-899-863A-2	Sequence 2, Appl
59	65.6	38.4	130	1	US-07-938-084-6	Sequence 6, Appl
60	64.6	37.8	171	1	US-07-858-124-19	Sequence 19, Appl
61	64.2	37.5	5829	3	US-09-439-311-473	Sequence 473, App
62	64.2	37.5	5829	4	US-09-636-215-473	Sequence 473, App
63	64.2	37.5	5829	4	US-09-685-166A-473	Sequence 473, App
64	64.2	37.5	5829	4	US-09-679-426-473	Sequence 473, App
65	64.2	37.5	5829	4	US-09-759-143-473	Sequence 473, App
66	64.2	37.5	5829	4	US-09-651-236-473	Sequence 473, App
67	62.6	36.6	100	1	US-07-938-084-11	Sequence 11, Appl
68	62.6	36.6	474	4	US-09-621-976-16748	Sequence 16748, A
69	57.2	33.5	146	4	US-09-513-999C-16140	Sequence 16140, A
70	54.8	32.0	174	1	US-07-858-124-21	Sequence 21, Appl
71	48.2	28.2	80	1	US-07-938-084-10	Sequence 10, Appl
72	48	28.1	192	1	US-08-153-051B-21	Sequence 21, Appl
73	48	28.1	192	1	US-08-060-955C-37	Sequence 37, Appl
74	48	28.1	192	2	US-08-151-477A-21	Sequence 21, Appl
75	48	28.1	192	3	US-08-819-867-51	Sequence 51, Appl
76	48	28.1	192	3	US-08-464-011B-37	Sequence 37, Appl
77	48	28.1	192	4	US-09-378-535-51	Sequence 51, Appl
78	38.4	22.5	80	3	US-09-308-759A-18	Sequence 18, Appl
79	37.2	21.8	60	1	US-07-938-084-9	Sequence 9, Appl
80	37.2	21.8	61	4	US-09-513-999C-27263	Sequence 27263, A
81	35.6	20.8	858	3	US-09-333-521-2	Sequence 2, Appl
82	35.6	20.8	858	4	US-09-899-863A-2	Sequence 2, Appl
83	35.4	20.7	190078	4	US-09-949-016-12707	Sequence 12707, A
84	35.4	20.7	190078	4	US-09-949-016-17026	Sequence 17026, A
85	35	20.5	252	4	US-09-513-999C-27943	Sequence 27943, A
86	34.4	20.1	177293	4	US-09-949-016-16513	Sequence 16513, A
87	33.6	19.6	50	2	US-08-832-468-5	Sequence 5, Appl
88	33.6	19.6	8550	4	US-09-949-016-1424	Sequence 1424, A
89	33.4	19.5	601	4	US-09-949-016-53880	Sequence 53880, A
90	33.4	19.5	75176	4	US-09-949-016-13300	Sequence 13300, A
91	33	19.3	231293	4	US-09-949-016-16110	Sequence 16110, A
92	33	19.3	266293	4	US-09-949-016-11934	Sequence 11934, A
93	32.6	18.7	601	4	US-09-949-016-156497	Sequence 156497, A
94	32	18.7	601	4	US-09-949-016-184461	Sequence 184461, A
95	30.6	17.9	601	4	US-09-949-016-184461	Sequence 184461, A
96	30.6	17.9	601	4	US-09-949-016-184465	Sequence 184465, A
97	30.2	17.7	5064	3	US-08-936-107A-8	Sequence 8, Appl
98	29.8	17.4	826	4	US-09-919-112-99	Sequence 99, Appl
99	29.8	17.4	826	4	US-09-976-594-811	Sequence 811, App
100	29.8	17.4	4821	3	US-08-913-374-1	Sequence 1, Appl

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:44:41 ; Search time 102.653 Seconds

(without alignments)
9861.108 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171

Sequence: 1 aattctcgtactctctctg.....ctatagaactagacagat 171

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :
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2: geneseg1980s:*
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5: geneseg2001as:*
6: geneseg2002as:*
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8: geneseg2004as:*
9: geneseg2005as:*
10: geneseg2006as:*
11: geneseg2007as:*
12: geneseg2008as:*
13: geneseg2009as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	171	7	AD830968 Human, gen
2	170.2	99.5	265	10	ACD93531 Human col
3	169	98.8	221	10	ACD93531 Human col
4	161.4	94.4	348	2	AA83284 Breast ca
5	161.4	94.4	348	2	AA83284 Breast ca
6	161.4	94.4	348	2	AA83284 Breast ca
7	161.4	94.4	348	2	AA83284 Breast ca
8	161.4	94.4	348	2	AA83284 Breast ca
9	161.4	94.4	348	2	AA83284 Breast ca
10	161.4	94.4	348	2	AA83284 Breast ca
11	150.2	87.8	824	8	ACC50969 Human bla
12	150.2	87.8	824	8	ACC50969 Human bla
13	150.2	87.8	824	8	ACC50969 Human bla
14	147	86.0	570	8	ACC50979 Human bla
15	145.4	85.0	458	12	ADQ20034 Human sof
16	145.4	85.0	458	12	ADQ20034 Human sof
17	145.4	85.0	458	12	ADQ20034 Human sof
18	142.2	83.2	570	12	ADQ25496 Human sof
19	139	81.3	464	13	ADK37535 Human alp
20	131.6	77.0	712	6	ABK27490 DNA encod

21	131.4	76.8	293	2	AA83285 Breast ca
22	131.4	76.8	293	2	AA83285 Breast ca
23	131.4	76.8	293	2	AA83285 Breast ca
24	131.4	76.8	293	2	AA83285 Breast ca
25	131.4	76.8	293	2	AA83285 Breast ca
26	131.4	76.8	293	2	AA83285 Breast ca
27	131.4	76.8	293	2	AA83285 Breast ca
28	116.2	68.0	312477	12	ADP65744 Human ROC
29	115.6	67.0	38062	4	AAK75209 Human imm
30	114.6	67.0	693	12	ACH87112 Human gen
31	113.2	66.2	717	13	ADR37541 Human alp
32	113	66.1	257	10	ACD97512 Human col
33	113	66.1	549	4	ABA62121 Human foe
34	113	66.1	549	4	ABA62121 Human foe
35	113	66.1	549	4	ABA62121 Human foe
36	112.6	65.8	351	3	AA83043 Human sec
37	111.4	65.1	360	3	AA83043 Human sec
38	111.4	65.1	534	9	ACH16911 Human adu
39	111.4	65.1	827	9	AD882448 Human CDN
40	111.4	65.1	850	6	AB889505 Human pro
41	111.4	65.1	1080	6	AD883056 Human CDN
42	111.4	65.1	2171	4	AAH18497 Human CDN
43	111.4	65.1	2186	12	ADQ63085 Novel Hum
44	110.8	64.8	340	10	ADP23572 Human lun
45	110.8	64.8	340	10	ADP23572 Human lun
46	110.8	64.8	340	10	ADP23572 Human lun
47	110.4	64.6	2026	5	AAI71672 Human myo
48	109.8	64.2	2847	10	AA849908 Human alp
49	108.8	63.6	2950	10	AA849909 Human alp
50	108.2	63.3	405	9	ACH16235 Human adu
51	108.2	63.3	546	4	AAK10382 Human bra
52	108.2	63.3	724	4	AAH05647 Human CDN
53	108.2	63.3	1741	12	ADQ20027 Human sof
54	108.2	63.3	1741	12	ADQ20027 Human sof
55	108.2	63.3	1868	2	AAV24221 Centromer
56	108.2	63.3	1868	2	AAV24221 Centromer
57	108.2	63.3	2056	10	AA849959 Human chr
58	108.2	63.3	2723	10	AA849960 Human chr
59	106.6	62.3	523	12	ACH73386 Human pro
60	106.6	62.3	542	5	AA80810 Human pro
61	106.6	62.3	611	4	AA830883 Human CDN
62	106.6	62.3	2546	1	AA806095 Fragment
63	106.6	62.0	1155	5	AA878015 DNA encod
64	106.6	62.0	2909	5	AA873293 DNA encod
65	105.2	61.5	357	2	AA861262 Human bra
66	105	61.4	341	10	AA849951 Human alp
67	105	61.4	514	12	ACH71629 Human gen
68	104.2	60.9	419	3	AA828742 Human sec
69	104.2	60.9	419	3	AA828742 Human sec
70	103.6	60.6	361	2	AA8059805 Human bra
71	103.4	60.5	541	12	ACH71431 Human gen
72	103.4	60.5	561	4	AA141324 Human bra
73	103.4	60.5	561	4	AA809714 Human bra
74	103.4	60.5	606	4	AA830912 Human CDN
75	102	59.6	309	4	AA876729 Human imm
76	101.8	59.5	339	2	AA876729 Human imm
77	101.8	59.5	339	2	AA876729 Human imm
78	101.8	59.5	339	2	AA876729 Human imm
79	101	59.1	1044	8	AD814732 Human hex
80	101	59.1	1044	8	AD814732 Human hex
81	101	59.1	1044	8	AD814732 Human hex
82	100.4	58.7	134	4	AA876727 Human imm
83	100	58.5	398	4	AA876732 Human imm
84	100	58.5	398	4	AA876732 Human imm
85	100	58.5	398	4	AA876732 Human imm
86	100	58.5	398	4	AA876732 Human imm
87	99.8	58.4	1044	8	ABX11071 DNA fragm
88	99.2	58.0	510	12	AA873118 Human gen
89	99.2	58.0	510	12	AA873118 Human gen
90	99	57.9	263	3	AA818447 Human pro
91	98.8	57.7	367	5	AB858247 Human pro
92	98.6	57.8	370	9	ACT05159 Retrovira
93	97.8	57.2	336	10	ADK11642 Breast ca

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 01:48:37 ; Search time 784.412 Seconds

(without alignments)
10563.118 Million cell updates/sec

Title: US-09-854-867-1

Perfect score: 171
Sequence: 1 aatctcagaactctctg.....ctatagaactagacagaat 171

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: gb_ba:*
2: gb_hng:*
3: gb_in:*
4: gb_cm:*
5: gb_cv:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	171	100.0	340 9 HUMSCNTM	M20434 Human alph
3	171	100.0	342 9 HUMSAT1	J00305 human tand
4	171	100.0	2 AL831785-7	Continuation (8 of
5	171	100.0	2 AC114775	AC114775 Homo sapi
6	171	100.0	2 AC104603	AC104603 Drosophi
7	169.4	99.1	171 9 HSAR1071	X13630 Human alph
8	169.4	99.1	171 9 HSAR1261	X13632 Human alph
9	169.4	99.1	340 9 HSPS3C	X60717 Human clone
10	169.4	99.1	685 9 HSA295044	AJ295044 Homo sapi
11	169.4	99.1	2 AC135046	AC135046 Homo sapi
12	169.4	99.1	321519 2 AL714004	AL714004 Homo sapi
13	168.4	98.5	280 9 HS286CR	Z55240 H. sapiens C
14	167.8	98.1	338 9 S49993	S49993 [R-DNA, alp
15	167.8	98.1	2 AC135046	AC135046 Homo sapi
16	167.8	98.1	2 AC104603	AC104603 Drosophi
17	166.2	97.2	171 9 HSAR31	X13633 Human alph
18	166.2	97.2	344 9 HUMSCNTU	M18124 Human alph
19	166.2	97.2	2 BX322633	BX322633 Homo sapi

22	166.2	97.2	163824 2	BX284928
23	165.8	97.0	171 9	HSREPI
24	165.8	97.0	277 9	HS90G9F
25	165.2	96.6	185887 2	AC133553
26	164.6	96.3	171 9	HSAR1341
27	164.6	96.3	340 9	HUMSCNTN
28	164.6	96.3	344 9	HUMSCNTI
29	164.6	96.3	171474 2	AC135053
30	163	95.3	171 9	HSAR201
31	163	95.3	171 9	HSAR51
32	163	95.3	171 9	HSAR61
33	163	95.3	346 9	HSAR295042
34	163	95.3	2	AC140814
35	161.4	94.4	171 9	HSAR1231
36	161.4	94.4	171 9	HSAR911
37	161.4	94.4	302 9	HS5CAF
38	161.4	94.4	344 9	HUMSCNTH
39	161.4	94.4	344 9	HUMSCNTK
40	161.4	94.4	348 6	AR147916
41	161.4	94.4	348 6	AR219640
42	161.4	94.4	348 6	AR350738
43	161.4	94.4	348 6	AR433114
44	161.4	94.4	348 6	AX316748
45	161.4	94.4	348 6	BD084231
46	161.4	94.4	680 9	HUMSATD
47	161.4	94.4	2	AC140816
48	161.4	94.4	2	AL391668
49	161.4	94.4	2	AL391668
50	159.8	93.5	171 9	HSAR21
51	159.8	93.5	171 9	HSAR81
52	159.8	93.5	644 9	AJ717298
53	159.8	93.5	2	AC140814
54	159.4	93.2	275 9	HS12B11F
55	158.6	92.7	159530 2	AC133922
56	158.2	92.5	171 9	HSAR1151
57	158.2	92.5	171 9	HUMSATL
58	158.2	92.5	348 9	HS6D10R
59	158.2	92.5	344 9	HUMSCNTG
60	156.8	91.7	279 9	HS30GAR
61	156.6	91.6	43705 9	AC010517
62	156.2	91.3	313 9	HS37A8R
63	155	90.6	166111 2	AC073442
64	154.6	89.4	275 9	HS18H3F
65	152.4	89.1	171 9	HUMSATP
66	148.6	86.9	3906 9	HS5ATAP
67	148.6	86.9	167060 2	AC141296
68	148.6	86.9	174688 9	AC026131
69	148.6	86.9	185972 2	AC069355
70	148.6	86.9	191752 9	BX322613
71	147	86.0	168763 9	AC146133
72	146.2	85.5	341 9	HUMSCNTT
73	146.2	85.5	1049 9	HUMSATAC
74	145.4	85.0	110000 2	AC148612_1
75	145.4	85.0	110000 2	AC148612_2
76	144.4	84.4	340 9	HUMSCNTU
77	144	84.2	336 9	HS26E1R
78	143.8	84.1	171 9	HUMSATK
79	143.8	84.1	334 9	S49988
80	143.8	84.1	3529 9	AC123578
81	143.8	84.1	69462 2	AC073925
82	143.8	84.1	187282 9	AC019063
83	142.4	83.3	172 9	HUMSATAG
84	142.2	83.2	33836 9	AC142529
85	142.2	83.2	110000 2	AL81785_2
86	142.2	83.2	153456 2	AC136945
87	142.2	83.2	158766 2	AC137793
88	142	83.0	308 9	HS43DSF
89	141	82.5	166 9	HUMARDNA
90	140.8	82.3	326 9	HS7D3R
91	140.6	82.2	343 9	HUMSCNTF
92	140.6	82.2	680 9	HUMSATV7C

BX284928	Homo sapi
V00579	Human repet
Z63828	H. sapiens C
AC133553	Homo sapi
X13636	Human alph
M20435	Human alph
M18123	Human alph
AC135053	Homo sapi
X13642	Human alph
X13645	Human alph
X13638	Human alph
AJ295042	Homo sapi
AC140814	Homo sapi
X13651	Human alph
X13647	Human alph
Z65792	H. sapiens C
M18122	Human alph
M21871	Human alph
AR147916	Sequence
AR219640	Sequence
AR350738	Sequence
AR433114	Sequence
AX316748	Sequence
BD084291	Compositi
M58446	Human alph
AC140816	Homo sapi
AL391668	Homo sapi
AL391668	Homo sapi
X13640	Human alph
X13649	Human alph
AJ717298	Homo sapi
AC140814	Homo sapi
Z56579	H. sapiens C
AC133922	Homo sapi
X13644	Human alph
M27772	Human alph
Z60841	H. sapiens C
M18121	Human alph
Z58181	H. sapiens C
AC010517	Homo sapi
Z55373	H. sapiens C
AC073442	Homo sapi
Z57696	H. sapiens C
M27778	Human alph
X67031	H. sapiens D
AC026131	Homo sapi
AC069355	Homo sapi
BX322613	Human DNA
AC146133	Par trogl
M20441	Human alph
M26920	Human alph
Continuation (2 of	
Continuation (3 of	
M20442	Human alph
Z58018	H. sapiens C
M27771	Human alph
S49988	[R-DNA, alp
AC123578	Homo sapi
AC073925	Homo sapi
AC019063	Homo sapi
M27777	Human alph
AC142529	Homo sapi
Continuation (3 of	
AC136945	Homo sapi
AC137793	Homo sapi
Z61072	H. sapiens C
M28426	Human alph
Z66184	H. sapiens C
M18120	Human alph
M16101	Human tetra